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Gerlach, Valerie  
MacDougall, John R  
Malyankar, Muriel M  
Smithson, Glennnda  
Millet, Isabelle  
Peyman, John A  
Stone, David J  
Gunther, Erik  
Ellerman, Karen  
Shimkets, Richard A  
Padigaru, Muralidhara  
Guo, Xiaojia  
Patturajan, Meera  
Taupier Jr, Raymond J  
Burgess, Catherine E  
Zerhusen, Bryan D  
Kekuda, Ramesh  
Spytek, Kimberly A  
Gangolli, Esha A  
Fernandes, Elma R  
Gorman, Linda

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His	Tyr	Lys	Trp	Lys	Pro	Tyr	Thr	Gln	Val	Glu	Gln	Asp	Leu	Cys	Lys	
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<211> 2902

<212> DNA

<213> Homo sapiens

<400> 5

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<211> 856

<212> PRT

<213> Homo sapiens

<400> 6

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Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala	370	375	380			
His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn	385	390	395	400		
Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly	405	410	415			
Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His	420	425	430			
Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys	435	440	445			
Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr	450	455	460			
Gly Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu	465	470	475	480		
Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His	485	490	495			
Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly	500	505	510			
Thr Ile Cys Gly His Glu His Gly Ala Gly Gly Gln Cys Val Lys Tyr	515	520	525			
Gly Asp Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp Ser	530	535	540			
Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His Arg	545	550	555	560		
Ser Arg Ser Gln Asn Thr His Ser Arg Pro Ser His Gly Gly Lys Phe	565	570	575			
Cys Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys	580	585	590			
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Leu	Ile	Ala	Thr	Gly	Pro	Thr	Asn	Glu	Thr	Leu	Ile	Val	Glu	Leu	Leu
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Phe	Gln	Gly	Arg	Asn	Pro	Gly	Val	Ala	Trp	Glu	Tyr	Ser	Met	Pro	Arg
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Leu	Gly	Thr	Glu	Lys	Gln	Pro	Pro	Ala	Gln	Pro	Ser	Tyr	Thr	Trp	Ala
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<211> 952

<212> PRT

<213> Homo sapiens

<400> 8

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Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu	Glu	
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1380 1385 1390

Pro Leu Val Lys Lys Val Glu Phe Gly Thr Asp Thr Leu Asn Ile Tyr  
1395 1400 1405

Leu Asp Glu Leu Ile Lys Asn Thr Gln Thr Tyr Thr Phe Thr Ile Ser  
1410 1415 1420

Gln Ser Val Leu Val Thr Asn Leu Lys Pro Ala Thr Ile Lys Val Tyr  
1425 1430 1435 1440

Asp Tyr Tyr Leu Pro Gly Ser Phe Lys Leu Ser Gln Tyr Thr Ile Val  
1445 1450 1455

Trp Ser Met Asn Asn Asp Ser Ile Val Asp Ser Val Ala Arg His Pro  
1460 1465 1470

Glu Pro Pro Pro Phe Lys Thr Glu Ala Phe Ile Pro Ser Leu Pro Gly  
1475 1480 1485

Ser Val Asn Asn  
1490

<210> 11  
<211> 987  
<212> DNA  
<213> Homo sapiens

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atgatggggc tgctcatggt ctctttggga tgttccgtgg agatccggaa gctgtgggtcg 180  
cacatcagga gacctgggg cattgctgtg ggactgctct gccagtttggt gctcatgcct 240  
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tcctggagtc ttcagcagaa tctcaccatt ccttatcaga acataggtct gtcttttagga 480  
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gcagttgctg gtgtgggtcct ggcgaaagga tcttggaatt cagacatcac ccttctgacc 660  
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caccagtctt ggcaaaggac cttgcctatc tttttagggt tagctttcaa gacaccctgt 780  
gataccctac tcgcaatgac ttcgtgtcct gaatgttcca ggctcatcta tgccttcatt 840

cctctgctat atggactctt ccagctgata gatggatttc ttattgttga agagagaaca 900  
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cctaaacaac ctaggatatg acagctt 987

<210> 12  
<211> 326  
<212> PRT  
<213> Homo sapiens

<400> 12

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Glu	Glu	Glu	Leu	Pro	Val	Gly	Leu	Glu	Val	His	Gly	Asn	Leu	Glu	Leu			
			20					25					30					
Val	Phe	Thr	Val	Val	Ser	Thr	Ile	Met	Met	Gly	Leu	Leu	Met	Phe	Ser			
			35				40					45						
Leu	Gly	Cys	Ser	Val	Glu	Ile	Arg	Lys	Leu	Trp	Ser	His	Ile	Arg	Arg			
	50					55					60							
Pro	Trp	Gly	Ile	Ala	Val	Gly	Leu	Leu	Cys	Gln	Phe	Gly	Leu	Met	Pro			
65					70					75					80			
Phe	Thr	Ala	Tyr	Leu	Leu	Ala	Ile	Ser	Phe	Ser	Leu	Lys	Pro	Val	Gln			
				85					90					95				
Ala	Ile	Ala	Val	Leu	Ile	Met	Gly	Cys	Cys	Arg	Gly	Ala	Pro	Ser	Leu			
			100					105					110					
Thr	Phe	Ser	Pro	Ser	Gly	Leu	Met	Glu	Ile	Trp	Ile	Ser	Gly	Ala	Leu			
		115					120					125						
Gly	Met	Met	Pro	Leu	Cys	Ile	Tyr	Leu	Tyr	Thr	Trp	Ser	Trp	Ser	Leu			
	130					135					140							
Gln	Gln	Asn	Leu	Thr	Ile	Pro	Tyr	Gln	Asn	Ile	Gly	Leu	Ser	Leu	Gly			
145					150					155					160			
Ile	Thr	Leu	Val	Cys	Leu	Thr	Ile	Pro	Val	Ala	Phe	Gly	Val	Tyr	Val			
				165					170					175				
Asn	Tyr	Arg	Trp	Pro	Lys	Gln	Ser	Lys	Ile	Ile	Leu	Lys	Ala	Val	Val			
			180					185					190					
Gly	Gly	Val	Leu	Leu	Leu	Val	Val	Ala	Val	Ala	Gly	Val	Val	Leu	Ala			
		195					200					205						
Lys	Gly	Ser	Trp	Asn	Ser	Asp	Ile	Thr	Leu	Leu	Thr	Ile	Ser	Phe	Ile			
	210					215					220							
Phe	Pro	Leu	Ile	Gly	His	Val	Thr	Gly	Phe	Leu	Leu	Ala	Leu	Phe	Thr			
225					230					235					240			
His	Gln	Ser	Trp	Gln	Arg	Thr	Leu	Pro	Ile	Phe	Leu	Gly	Leu	Ala	Phe			

				245						250						255			
Lys	Thr	Pro	Cys	Asp	Thr	Leu	Leu	Ala	Met	Thr	Ser	Cys	Pro	Glu	Cys				
			260					265					270						
Ser	Arg	Leu	Ile	Tyr	Ala	Phe	Ile	Pro	Leu	Leu	Tyr	Gly	Leu	Phe	Gln				
		275					280					285							
Leu	Ile	Asp	Gly	Phe	Leu	Ile	Val	Glu	Glu	Arg	Thr	Glu	Asp	Thr	Asp				
	290					295					300								
Cys	Asp	Gly	Ser	Pro	Leu	Pro	Glu	Tyr	Phe	Thr	Glu	Val	Thr	Ile	Ile				
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Pro	Lys	Gln	Pro	Arg	Ile														
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<210> 13  
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 <212> DNA  
 <213> Homo sapiens

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 ttgaccgatt ccgtggagt caggacattg tggtaggcaa agggactcac tgtctcatcc 180  
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 cgccgtccat cacgaacaag atcctcaagt cagtgggtggc tcgctttgaa gctggagaac 420  
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 ccacctttgg gctcattctg gacgacgtgt ccttgacata tctgaccttc gggaaggagt 540  
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 tgggtggaaa ggctgagcag cagaaaaagg cggccatcat ttctgctgag ggcgactcca 660  
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 gcaagctgga agctgtggag gacatcacct accagctttt acgctctcgg aacatcacct 780  
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 cacctccgag 850

<210> 14  
 <211> 272  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
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 20 25 30  
 Gly His Arg Ala Val Val Phe Asp Arg Phe Arg Gly Val Gln Asp Ile  
 35 40 45  
 Val Val Gly Lys Gly Thr His Cys Leu Ile Pro Trp Leu Gln Lys Ser

50	55	60
Ile Ile Phe Asp Cys Arg Ser Gln Pro Arg Asn Val Pro Val Ile Thr		
65	70	75 80
Gly Ser Lys Asp Leu Gln Asn Val Asn Leu Thr Leu Arg Ile Ile Phe		
	85	90 95
Arg Pro Val Ala Ser Gln Leu Pro His Ile Phe Thr Ser Ser Gly Glu		
	100	105 110
Asp His Asp Glu Arg Val Pro Pro Ser Ile Thr Asn Lys Ile Leu Lys		
	115	120 125
Ser Val Val Ala Arg Phe Glu Ala Gly Glu Leu Ile Thr Gln Arg Glu		
	130	135 140
Gln Ile Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Pro Ala Ala Thr		
	145	150 155 160
Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr Leu Thr Phe Gly		
	165	170 175
Lys Glu Phe Ile Glu Ala Val Glu Ala Lys Gln Ile Ala Gln Gln Glu		
	180	185 190
Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys		
	195	200 205
Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Val Ala Glu Leu Ile		
	210	215 220
Thr Asn Ser Leu Ala Thr Ala Gly Asp Ala Leu Ile Glu Leu Arg Lys		
	225	230 235 240
Leu Glu Ala Val Glu Asp Ile Thr Tyr Gln Leu Leu Arg Ser Arg Asn		
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Ile Thr Tyr Leu Arg Ala Gly Gln Ser Met Pro Leu Gln Leu Arg Trp		
	260	265 270

<210> 15  
 <211> 2011  
 <212> DNA  
 <213> Homo sapiens

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 gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg ttgccaactg 240  
 ctgccatgga ctcaacactc gccccacacg aggctgcggc gttctgggcg ctgtgacctc 300  
 ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg gtaccggggc 360



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aaggtcatga gactgggtta ggcccagcct t 2011

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<210> 16

<211> 666

<212> PRT

<213> Homo sapiens

<400> 16

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Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
      20              25              30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
      35              40              45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
      50              55              60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
      65              70              75              80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
      85              90              95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
      100              105              110

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Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly	
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Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr	
	130					135					140					
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	
145					150					155					160	
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	
				165					170					175		
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	
			180					185					190			
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	
	195						200					205				
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	
	210					215					220					
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	
225					230					235					240	
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	
				245					250					255		
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	
			260					265					270			
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	
		275					280					285				
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	
	290					295					300					
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	
305					310					315					320	
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	
				325					330					335		
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	
			340					345					350			
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	
		355					360					365				
Thr	Ala	Thr	Thr	Ala	Gln	Gly	Ser	Ser	Thr	Ala	Ala	Arg	Ser	Ala	Arg	
	370					375					380					
Pro	Ala	Arg	Val	Ser	Ser	Ala	Ser	Ala	Gly	Pro	Leu	Arg	Arg	Arg	Thr	
385					390					395					400	
Ser	Arg	Ser	Ser	Arg	Leu	Pro	Pro	Asn	Arg	Met	His	Asn	Trp	Arg	Arg	
				405					410					415		

Thr Ser Ala Gly Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala Thr  
 420 425 430  
 Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala Ala  
 435 440 445  
 Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys Ser  
 450 455 460  
 Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Gly Val Pro  
 465 470 475 480  
 Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln Ser  
 485 490 495  
 Ala Cys Gly Ile Gly Met Leu Pro Leu Thr Gly Tyr Glu Val Trp Leu  
 500 505 510  
 Gly Thr Leu Phe Gln Asn Pro Gln His Gly Glu Pro Ser Leu Gln Arg  
 515 520 525  
 Val Pro Val Ala Lys Met Val Cys Gly Pro Ser Gly Ser Gln Leu Val  
 530 535 540  
 Leu Leu Lys Leu Glu Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu  
 545 550 555 560  
 Ile Cys Leu Pro Pro Glu Trp Tyr Val Val Pro Pro Gly Thr Lys Cys  
 565 570 575  
 Glu Ile Ala Gly Trp Gly Glu Thr Lys Gly Thr Gly Asn Asp Thr Val  
 580 585 590  
 Leu Asn Val Ala Leu Leu Asn Val Ile Ser Asn Gln Glu Cys Asn Ile  
 595 600 605  
 Lys His Arg Gly Arg Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr  
 610 615 620  
 His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys  
 625 630 635 640  
 Ala Arg Ser Cys Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val  
 645 650 655  
 Asp Trp Ile His Lys Val Met Arg Leu Gly  
 660 665

<210> 17  
 <211> 634  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
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 gccacagttc agcagctggg aggaagatgg cgcctggtgg acagcaaacg ctttgatgaa 120

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tacatgaagg agggaggagt gggaaactgct ttgcgaaaaa tggacgcaat ggccaagcca 180
gattgtatca tcacttgtga tggcaaaaac ctcaccataa aaaccgagag cactttgaaa 240
acacagtttt cttgtaccct gggagagaag tttgaagaaa ccacagctga tggcagaaaa 300
actcagactg tgtgcagctt tgcagatggg gcattgggtc agcatcagga gtgggatggg 360
aaggaaaaca caataacaag aaaactgaaa gatgggaaat tagtggtgta ctgtgtcatg 420
aacaatgtcg cctgtactcg gatctatgaa aaagtagaat aaaaattcca tcatcacttt 480
ggacaggagt taactaatag aatgatcaag ctcagttcaa tgagcaaadc tccatagtgt 540
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aagtgtcttg gattaattag gatcatccct ttgg 634

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<210> 18  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

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<400> 18
Met Ala Thr Val Gln Gln Leu Gly Gly Arg Trp Arg Leu Val Asp Ser
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Lys Arg Phe Asp Glu Tyr Met Lys Glu Gly Gly Val Gly Thr Ala Leu
      20             25            30

Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
      35             40            45

Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe
      50             55            60

Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg
      65             70            75            80

Lys Thr Gln Thr Val Cys Ser Phe Ala Asp Gly Ala Leu Val Gln His
      85             90            95

Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp
      100            105           110

Gly Lys Leu Val Val Tyr Cys Val Met Asn Asn Val Ala Cys Thr Arg
      115            120           125

Ile Tyr Glu Lys Val Glu
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<210> 19  
 <211> 822  
 <212> DNA  
 <213> Homo sapiens

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ccccaacgtc tgctatgacg agttcttccc cgtgtcccac gtgcgcctct gggccctaca 240
gctcatcctg gtcaagtgcc cctcactgct cgtgggtcat cagtggcct accgcgagga 300
acgcgagcgc aagcaccacc tgaaacacgg gcccaatgcc ccgtccctgt acgacaacct 360

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gagcaagaag cggggcggac tgtggtggac gtacttgctg agcctcatct tcaaggccgc 420
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cgtggtggcc tgctccgtgg agccttgccc ccacactgtg gactgttaca tctcccggcc 540
cacggagaag aaggtcttca cctacttcat ggtgaccaca gctgccatct gcatcctgct 600
caacctcagt gaagtcttct acctggtggg caagaggtgc atggagatct tcggccccag 660
gcaccggcgg cctcggtgcc gggaatgcct acccgatacg tgcccacat atgtcctctc 720
ccagggaggg caccctgagg atgggaactc tgtcctaata aaggctgggt cggccccagt 780
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<210> 20

<211> 266

<212> PRT

<213> Homo sapiens

<400> 20

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Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
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Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
      20              25              30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
      35              40              45

Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
      50              55              60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
      65              70              75              80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
      85              90              95

Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
      100             105             110

Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
      115             120             125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
      130             135             140

Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
      145             150             155             160

Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
      165             170             175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
      180             185             190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
      195             200             205

Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
      210             215             220

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Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser  
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Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly  
 245 250 255

Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro  
 260 265

<210> 21  
 <211> 546  
 <212> DNA  
 <213> Homo sapiens

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 tgtgaactaa atccacagcc acataataat caaaacagaa aagcaaaaaga aagccacttc 180  
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<210> 23  
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<210> 24

<211> 547

<212> PRT

<213> Homo sapiens

<400> 24

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Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn
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Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg			
			340					345					350					



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 385 390 395 400  
 Asp Arg Leu Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu  
 405 410 415  
 Val Glu Gly Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp  
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 <212> DNA  
 <213> Homo sapiens

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<210> 26

<211> 1787

<212> DNA

<213> Homo sapiens

<400> 26

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1787

<210> 27

<211> 472

<212> PRT

<213> Homo sapiens

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Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly
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Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly
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Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile
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Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln
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Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly
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Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys
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Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro
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Val	Ser	Leu	Arg	Cys	Ser	Glu	Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg
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 Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser Trp  
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<211> 2148

<212> DNA

<213> Homo sapiens

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ctgagggatg  agggggagga  gagaggtagg  agctggagat  gaagagactg  ctagaagcag  1740
caggaagcct  gcccttctgc  cctctccct  ccctgcccc  gtgtgagtct  tttagggagg  1800
gtgactggga  ggtgcccccc  gtcccacctt  tttcctgtgc  tctaggtggg  ctaagtgcct  1860
ccctagagga  ctccatggct  gagaggctcc  tgggcagatg  ggggtcaaggc  tgggccagtc  1920
ccagatgaag  cctatgggag  tcaggaccct  ctccactctc  cctctccact  ccccttccctg  1980
ttctcacctg  gctgtggctg  gccctgtgtg  ggggtgggtac  actggaaaac  aagaaggttg  2040
gagttggtct  aggacattgg  ttttaaata  cagttctgtg  aactggtcca  aggaggttct  2100
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<210> 29

<211> 418

<212> PRT

<213> Homo sapiens

<400> 29

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Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
  1             5             10             15

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```

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
      20             25             30

```

```

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
      35             40             45

```

```

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
      50             55             60

```

```

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
      65             70             75             80

```

```

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
      85             90             95

```

```

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
      100            105            110

```

Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln			
		115					120					125						
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly			
	130					135					140							
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys			
145					150					155					160			
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala			
				165					170					175				
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro			
			180					185					190					
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu			
		195					200					205						
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val			
	210					215					220							
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg			
225					230					235					240			
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala			
				245					250					255				
Ala	His	Cys	Met	His	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu			
			260					265					270					
Leu	Arg	Leu	Gln	Thr	Ala	Leu	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val			
	275						280					285						
Cys	Leu	Pro	Ala	Lys	Glu	Gln	His	Phe	Pro	Lys	Gly	Ser	Arg	Cys	Trp			
	290					295					300							
Val	Ser	Gly	Trp	Cys	His	Thr	His	Pro	Ser	His	Thr	Tyr	Ser	Ser	Asp			
305					310					315					320			
Met	Leu	Gln	Asp	Thr	Val	Val	Pro	Leu	Leu	Ser	Thr	Gln	Leu	Cys	Asn			
				325					330					335				
Ser	Ser	Cys	Val	Tyr	Ser	Gly	Ala	Leu	Thr	Pro	Arg	Met	Leu	Cys	Ala			
			340					345					350					
Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly			
	355						360					365						
Pro	Leu	Val	Cys	Pro	Asp	Gly	Asp	Thr	Trp	Arg	Leu	Val	Gly	Val	Val			
	370					375					380							
Ser	Trp	Gly	Arg	Gly	Cys	Ala	Glu	Pro	Asn	His	Pro	Gly	Val	Tyr	Ala			
385					390					395					400			
Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile	His	Asp	Thr	Ala	Gln	Asp	Ser			
				405					410					415				

Leu Leu

<210> 30  
<211> 1593  
<212> PRT  
<213> Homo sapiens

<400> 30

Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala  
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Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro  
20 25 30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly  
35 40 45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly  
50 55 60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg  
65 70 75 80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser  
85 90 95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe  
100 105 110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His  
115 120 125

Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr  
130 135 140

Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys  
145 150 155 160

His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile  
165 170 175

Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His  
180 185 190

Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys  
195 200 205

Gly Leu Lys Asp Ser Val Asn Ile Ser Gln Lys Gln Glu Leu Trp Arg  
210 215 220

Glu Lys Trp Glu Arg His Asn Leu Pro Ser Arg Ser Leu Ser Arg Arg  
225 230 235 240

Ser Ile Ser Lys Glu Arg Trp Val Glu Thr Leu Val Val Ala Asp Thr  
245 250 255

Lys	Met	Ile	Glu	Tyr	His	Gly	Ser	Glu	Asn	Val	Glu	Ser	Tyr	Ile	Leu	260	265	270
Thr	Ile	Met	Asn	Met	Val	Thr	Gly	Leu	Phe	His	Asn	Pro	Ser	Ile	Gly	275	280	285
Asn	Ala	Ile	His	Ile	Val	Val	Val	Arg	Leu	Ile	Leu	Leu	Glu	Glu	Glu	290	295	300
Glu	Gln	Gly	Leu	Lys	Ile	Val	His	His	Ala	Glu	Lys	Thr	Leu	Ser	Ser	305	310	315
Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Asn	Pro	Lys	Ser	Asp	Leu	Asn	Pro	325	330	335
Val	His	His	Asp	Val	Ala	Val	Leu	Leu	Thr	Arg	Lys	Asp	Ile	Cys	Ala	340	345	350
Gly	Phe	Asn	Arg	Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Leu	Ser	Gly	355	360	365
Met	Cys	Gln	Pro	His	Arg	Ser	Cys	Asn	Ile	Asn	Glu	Asp	Ser	Gly	Leu	370	375	380
Pro	Leu	Ala	Phe	Thr	Ile	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	385	390	395
Gln	His	Asp	Gly	Lys	Glu	Asn	Asp	Cys	Glu	Pro	Val	Gly	Arg	His	Pro	405	410	415
Tyr	Ile	Met	Ser	Arg	Gln	Leu	Gln	Tyr	Asp	Pro	Thr	Pro	Leu	Thr	Trp	420	425	430
Ser	Lys	Cys	Ser	Glu	Glu	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	435	440	445
Gly	Phe	Cys	Leu	Asp	Asp	Ile	Pro	Lys	Lys	Lys	Gly	Leu	Lys	Ser	Lys	450	455	460
Val	Ile	Ala	Pro	Gly	Val	Ile	Tyr	Asp	Val	His	His	Gln	Cys	Gln	Leu	465	470	475
Gln	Tyr	Gly	Pro	Asn	Ala	Thr	Phe	Cys	Gln	Glu	Val	Glu	Asn	Val	Cys	485	490	495
Gln	Thr	Leu	Trp	Cys	Ser	Val	Lys	Gly	Phe	Cys	Arg	Ser	Lys	Leu	Asp	500	505	510
Ala	Ala	Ala	Asp	Gly	Thr	Gln	Cys	Gly	Glu	Lys	Lys	Trp	Cys	Met	Ala	515	520	525
Gly	Lys	Cys	Ile	Thr	Val	Gly	Lys	Lys	Pro	Glu	Ser	Ile	Pro	Gly	Gly	530	535	540
Trp	Gly	Arg	Trp	Ser	Pro	Trp	Ser	His	Cys	Ser	Arg	Thr	Cys	Gly	Ala	545	550	555
																		560



Gly	Val	Gln	Ser	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Pro	Glu	Pro	Lys	Phe	
				565					570					575		
Gly	Gly	Lys	Tyr	Cys	Thr	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Leu	Cys	Asn	
			580					585					590			
Val	His	Pro	Cys	Arg	Ser	Glu	Ala	Pro	Thr	Phe	Arg	Gln	Met	Gln	Cys	
		595					600					605				
Ser	Glu	Phe	Asp	Thr	Val	Pro	Tyr	Lys	Asn	Glu	Leu	Tyr	His	Trp	Phe	
	610					615					620					
Pro	Ile	Phe	Asn	Pro	Ala	His	Pro	Cys	Glu	Leu	Tyr	Cys	Arg	Pro	Ile	
625					630					635					640	
Asp	Gly	Gln	Phe	Ser	Glu	Lys	Met	Leu	Asp	Ala	Val	Ile	Asp	Gly	Thr	
				645					650					655		
Pro	Cys	Phe	Glu	Gly	Gly	Asn	Ser	Arg	Asn	Val	Cys	Ile	Asn	Gly	Ile	
			660					665					670			
Cys	Lys	Met	Val	Gly	Cys	Asp	Tyr	Glu	Ile	Asp	Ser	Asn	Ala	Thr	Glu	
		675					680					685				
Asp	Arg	Cys	Gly	Val	Cys	Leu	Gly	Asp	Gly	Ser	Ser	Cys	Gln	Thr	Val	
	690					695					700					
Arg	Lys	Met	Phe	Lys	Gln	Lys	Glu	Gly	Ser	Gly	Tyr	Val	Asp	Ile	Gly	
705					710				715					720		
Leu	Ile	Pro	Lys	Gly	Ala	Arg	Asp	Ile	Arg	Val	Met	Glu	Ile	Glu	Gly	
			725					730					735			
Ala	Gly	Asn	Phe	Leu	Ala	Ile	Arg	Ser	Glu	Asp	Pro	Glu	Lys	Tyr	Tyr	
			740					745					750			
Leu	Asn	Gly	Gly	Phe	Ile	Ile	Gln	Trp	Asn	Gly	Asn	Tyr	Lys	Leu	Ala	
		755					760					765				
Gly	Thr	Val	Phe	Gln	Tyr	Asp	Arg	Lys	Gly	Asp	Leu	Glu	Lys	Leu	Met	
	770					775					780					
Ala	Thr	Gly	Pro	Thr	Asn	Glu	Ser	Val	Trp	Ile	Gln	Leu	Leu	Phe	Gln	
785					790					795					800	
Val	Thr	Asn	Pro	Gly	Ile	Lys	Tyr	Glu	Tyr	Thr	Ile	Gln	Lys	Asp	Gly	
			805					810						815		
Leu	Asp	Asn	Asp	Val	Glu	Gln	Met	Tyr	Phe	Trp	Gln	Tyr	Gly	His	Trp	
			820					825					830			
Thr	Glu	Cys	Ser	Val	Thr	Cys	Gly	Thr	Gly	Ile	Arg	Arg	Gln	Thr	Ala	
		835					840					845				
His	Cys	Ile	Lys	Lys	Gly	Arg	Gly	Met	Val	Lys	Ala	Thr	Phe	Cys	Asp	
	850					855					860					

Pro Glu Thr Gln Pro Asn Gly Arg Gln Lys Lys Cys His Glu Lys Ala  
 865 870 875 880  
 Cys Pro Pro Arg Trp Trp Ala Gly Glu Trp Glu Ala Cys Ser Ala Thr  
 885 890 895  
 Cys Gly Pro His Gly Glu Lys Lys Arg Thr Val Leu Cys Ile Gln Thr  
 900 905 910  
 Met Val Ser Asp Glu Gln Ala Leu Pro Pro Thr Asp Cys Gln His Leu  
 915 920 925  
 Leu Lys Pro Lys Thr Leu Leu Ser Cys Asn Arg Asp Ile Leu Cys Pro  
 930 935 940  
 Ser Asp Trp Thr Val Gly Asn Trp Ser Glu Cys Ser Val Ser Cys Gly  
 945 950 955 960  
 Gly Gly Val Arg Ile Arg Ser Val Thr Cys Ala Lys Asn His Asp Glu  
 965 970 975  
 Pro Cys Asp Val Thr Arg Lys Pro Asn Ser Arg Ala Leu Cys Gly Leu  
 980 985 990  
 Gln Gln Cys Pro Ser Ser Arg Arg Val Leu Lys Pro Asn Lys Gly Thr  
 995 1000 1005  
 Ile Ser Asn Gly Lys Asn Pro Pro Thr Leu Lys Pro Val Pro Pro Pro  
 1010 1015 1020  
 Thr Ser Arg Pro Arg Met Leu Thr Thr Pro Thr Gly Pro Glu Ser Met  
 1025 1030 1035 1040  
 Ser Thr Ser Thr Pro Ala Ile Ser Ser Pro Ser Pro Thr Thr Ala Ser  
 1045 1050 1055  
 Lys Glu Gly Asp Leu Gly Gly Lys Gln Trp Gln Asp Ser Ser Thr Gln  
 1060 1065 1070  
 Pro Glu Leu Ser Ser Arg Tyr Leu Ile Ser Thr Gly Ser Thr Ser Gln  
 1075 1080 1085  
 Pro Ile Leu Thr Ser Gln Ser Leu Ser Ile Gln Pro Ser Glu Glu Asn  
 1090 1095 1100  
 Val Ser Ser Ser Asp Thr Gly Pro Thr Ser Glu Gly Gly Leu Val Ala  
 1105 1110 1115 1120  
 Thr Thr Thr Ser Gly Ser Gly Leu Ser Ser Ser Arg Asn Pro Ile Thr  
 1125 1130 1135  
 Trp Pro Val Thr Pro Phe Tyr Asn Thr Leu Thr Lys Gly Pro Glu Met  
 1140 1145 1150  
 Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys  
 1155 1160 1165

Asp	Glu	Ser	Asn	Pro	Val	Ile	Trp	Thr	Lys	Ile	Arg	Val	Pro	Gly	Asn	1170	1175	1180	
Asp	Ala	Pro	Val	Glu	Ser	Thr	Glu	Met	Pro	Leu	Ala	Pro	Pro	Leu	Thr	1185	1190	1195	1200
Pro	Asp	Leu	Ser	Arg	Glu	Ser	Trp	Trp	Pro	Pro	Phe	Ser	Thr	Val	Met	1205	1210	1215	
Glu	Gly	Leu	Leu	Pro	Ser	Gln	Arg	Pro	Thr	Thr	Ser	Glu	Thr	Gly	Thr	1220	1225	1230	
Pro	Arg	Val	Glu	Gly	Met	Val	Thr	Glu	Lys	Pro	Ala	Asn	Thr	Leu	Leu	1235	1240	1245	
Pro	Leu	Gly	Gly	Asp	His	Gln	Pro	Glu	Pro	Ser	Gly	Lys	Thr	Ala	Asn	1250	1255	1260	
Arg	Asn	His	Leu	Lys	Leu	Pro	Asn	Asn	Met	Asn	Gln	Thr	Lys	Ser	Ser	1265	1270	1275	1280
Glu	Pro	Val	Leu	Thr	Glu	Glu	Asp	Ala	Thr	Ser	Leu	Ile	Thr	Glu	Gly	1285	1290	1295	
Phe	Leu	Leu	Asn	Ala	Ser	Asn	Tyr	Lys	Gln	Leu	Thr	Asn	Gly	His	Gly	1300	1305	1310	
Ser	Ala	His	Trp	Ile	Val	Gly	Asn	Trp	Ser	Glu	Cys	Ser	Thr	Thr	Cys	1315	1320	1325	
Gly	Leu	Gly	Ala	Tyr	Trp	Lys	Arg	Val	Glu	Cys	Thr	Thr	Gln	Met	Asp	1330	1335	1340	
Ser	Asp	Cys	Ala	Ala	Ile	Gln	Arg	Pro	Asp	Pro	Ala	Lys	Arg	Cys	His	1345	1350	1355	1360
Leu	Arg	Pro	Cys	Ala	Gly	Trp	Lys	Val	Gly	Asn	Trp	Ser	Lys	Cys	Ser	1365	1370	1375	
Arg	Asn	Cys	Ser	Gly	Gly	Phe	Lys	Ile	Arg	Glu	Ile	Gln	Cys	Val	Asp	1380	1385	1390	
Ser	Arg	Asp	His	Arg	Asn	Leu	Arg	Pro	Phe	His	Cys	Gln	Phe	Leu	Ala	1395	1400	1405	
Gly	Ile	Pro	Pro	Pro	Leu	Ser	Met	Ser	Cys	Asn	Pro	Glu	Pro	Cys	Glu	1410	1415	1420	
Ala	Trp	Gln	Val	Glu	Pro	Trp	Ser	Gln	Cys	Ser	Arg	Ser	Cys	Gly	Gly	1425	1430	1435	1440
Gly	Val	Gln	Glu	Arg	Gly	Val	Phe	Cys	Pro	Gly	Gly	Leu	Cys	Asp	Trp	1445	1450	1455	
Thr	Lys	Arg	Pro	Thr	Ser	Thr	Met	Ser	Cys	Asn	Glu	His	Leu	Cys	Cys	1460	1465	1470	

His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly  
 1475 1480 1485  
 Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys  
 1490 1495 1500  
 Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro  
 1505 1510 1515 1520  
 Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu  
 1525 1530 1535  
 Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys  
 1540 1545 1550  
 Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe  
 1555 1560 1565  
 Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln  
 1570 1575 1580  
 Arg Leu Leu Gln Lys Ser Lys Glu Leu  
 1585 1590

<210> 31  
 <211> 1077  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
 Arg Ser Gln Asp Glu Phe Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala  
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 Phe Pro Thr Arg Val Asp His Asn Gly Ala Leu Leu Ala Phe Ser Pro  
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 Pro Pro Pro Arg Arg Gln Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser  
 35 40 45  
 Arg Leu Phe Tyr Lys Val Ala Ser Pro Ser Thr His Phe Leu Leu Asn  
 50 55 60  
 Leu Thr Arg Ser Ser Arg Leu Leu Ala Gly His Val Ser Val Glu Tyr  
 65 70 75 80  
 Trp Thr Arg Glu Gly Leu Ala Trp Gln Arg Ala Ala Arg Pro His Cys  
 85 90 95  
 Leu Tyr Ala Gly His Leu Gln Gly Gln Ala Ser Ser Ser His Val Ala  
 100 105 110  
 Ile Ser Thr Cys Gly Gly Leu His Gly Leu Ile Val Ala Asp Glu Glu  
 115 120 125  
 Glu Tyr Leu Ile Glu Pro Leu His Gly Gly Pro Lys Gly Ser Arg Ser

130		135		140													
Pro	Glu	Glu	Ser	Gly	Pro	His	Val	Val	Tyr	Lys	Arg	Ser	Ser	Leu	Arg		
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His	Pro	His	Leu	Asp	Thr	Ala	Cys	Gly	Val	Arg	Asp	Glu	Lys	Pro	Trp		
				165					170					175			
Lys	Gly	Arg	Pro	Trp	Trp	Leu	Arg	Thr	Leu	Lys	Pro	Pro	Pro	Ala	Arg		
			180					185					190				
Pro	Leu	Gly	Asn	Glu	Thr	Glu	Arg	Gly	Gln	Pro	Gly	Leu	Lys	Arg	Ser		
		195					200					205					
Val	Ser	Arg	Glu	Arg	Tyr	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Lys	Met		
	210					215					220						
Met	Val	Ala	Tyr	His	Gly	Arg	Arg	Asp	Val	Glu	Gln	Tyr	Val	Leu	Ala		
225					230					235					240		
Ile	Met	Asn	Ile	Val	Ala	Lys	Leu	Phe	Gln	Asp	Ser	Ser	Leu	Gly	Ser		
				245					250					255			
Thr	Val	Asn	Ile	Leu	Val	Thr	Arg	Leu	Ile	Leu	Leu	Thr	Glu	Asp	Gln		
			260					265						270			
Pro	Thr	Leu	Glu	Ile	Thr	His	His	Ala	Gly	Lys	Ser	Leu	Asp	Ser	Phe		
		275					280					285					
Cys	Lys	Trp	Gln	Lys	Ser	Ile	Val	Asn	His	Ser	Gly	His	Gly	Asn	Ala		
	290					295					300						
Ile	Pro	Glu	Asn	Gly	Val	Ala	Asn	His	Asp	Thr	Ala	Val	Leu	Ile	Thr		
305					310					315					320		
Arg	Tyr	Asp	Ile	Cys	Ile	Tyr	Lys	Asn	Lys	Pro	Cys	Gly	Thr	Leu	Gly		
				325					330					335			
Leu	Ala	Pro	Val	Gly	Gly	Met	Cys	Glu	Arg	Glu	Arg	Ser	Cys	Ser	Val		
			340					345					350				
Asn	Glu	Asp	Ile	Gly	Leu	Pro	Gln	Ala	Phe	Thr	Ile	Ala	His	Glu	Ile		
		355					360					365					
Gly	His	Thr	Phe	Gly	Met	Asn	His	Asp	Gly	Val	Gly	Asn	Ser	Cys	Gly		
	370					375					380						
Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	Met		
385					390					395					400		
Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Asn	Arg	Asp	Tyr	Ile	Thr		
				405					410					415			
Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	Pro		
			420					425					430				
Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	Asp		

435		440		445													
Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	Cys		
450						455					460						
Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	Asn		
465					470					475					480		
Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	Gln		
				485					490					495			
Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	Pro		
			500					505					510				
Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	Thr		
	515						520					525					
Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	Ser		
	530					535					540						
Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	Cys		
545					550					555					560		
Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	Pro		
				565					570					575			
Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	Ser		
			580					585					590				
Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	Gly		
	595						600					605					
Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Ser	Leu	Ala	Glu	Gly	Phe	Asn	Phe		
	610					615					620						
Tyr	Thr	Glu	Arg	Ala	Ala	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Arg	Pro		
625					630					635					640		
Asp	Thr	Val	Asp	Ile	Cys	Val	Ser	Gly	Glu	Cys	Lys	His	Val	Gly	Cys		
				645					650					655			
Asp	Arg	Val	Leu	Gly	Ser	Asp	Leu	Arg	Glu	Asp	Lys	Cys	Arg	Val	Cys		
		660						665					670				
Gly	Gly	Asp	Gly	Ser	Ala	Cys	Glu	Thr	Ile	Glu	Gly	Val	Phe	Ser	Pro		
	675						680					685					
Ala	Ser	Pro	Gly	Ala	Gly	Tyr	Glu	Asp	Val	Val	Trp	Ile	Pro	Lys	Gly		
	690					695					700						
Ser	Val	His	Ile	Phe	Ile	Gln	Asp	Leu	Asn	Leu	Ser	Leu	Ser	His	Leu		
705					710					715					720		
Ala	Leu	Lys	Gly	Asp	Gln	Glu	Ser	Leu	Leu	Leu	Glu	Gly	Leu	Pro	Gly		
			725						730					735			
Thr	Pro	Gln	Pro	His	Arg	Leu	Pro	Leu	Ala	Gly	Thr	Thr	Phe	Gln	Leu		

740						745						750					
Arg	Gln	Gly	Pro	Asp	Gln	Val	Gln	Ser	Leu	Glu	Ala	Leu	Gly	Pro	Ile		
		755					760					765					
Asn	Ala	Ser	Leu	Ile	Val	Met	Val	Leu	Ala	Arg	Thr	Glu	Leu	Pro	Ala		
		770				775					780						
Leu	Arg	Tyr	Arg	Phe	Asn	Ala	Pro	Ile	Ala	Arg	Asp	Ser	Leu	Pro	Pro		
785					790					795					800		
Tyr	Ser	Trp	His	Tyr	Ala	Pro	Trp	Thr	Lys	Cys	Ser	Ala	Gln	Cys	Ala		
				805					810					815			
Gly	Gly	Ser	Gln	Val	Gln	Ala	Val	Glu	Cys	Arg	Asn	Gln	Leu	Asp	Ser		
			820					825					830				
Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	Lys		
		835					840					845					
Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	Val		
		850				855						860					
Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	Ser		
865					870					875					880		
Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	Ala		
				885					890					895			
Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	Ala		
			900					905					910				
Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	Ser		
		915						920				925					
Glu	Cys	Thr	Pro	Ser	Cys	Gly	Pro	Gly	Leu	Arg	His	Arg	Val	Val	Leu		
		930				935					940						
Cys	Lys	Ser	Ala	Asp	His	Arg	Ala	Thr	Leu	Pro	Pro	Ala	His	Cys	Ser		
945					950					955					960		
Pro	Ala	Ala	Lys	Pro	Pro	Ala	Thr	Met	Arg	Cys	Asn	Leu	Arg	Arg	Cys		
				965					970					975			
Pro	Pro	Ala	Arg	Trp	Val	Ala	Gly	Glu	Trp	Gly	Glu	Cys	Ser	Ala	Gln		
			980					985					990				
Cys	Gly	Val	Gly	Gln	Arg	Gln	Arg	Ser	Val	Arg	Cys	Thr	Ser	His	Thr		
		995					1000				1005						
Gly	Gln	Ala	Ser	His	Glu	Cys	Thr	Glu	Ala	Leu	Arg	Pro	Pro	Thr	Thr		
		1010				1015					1020						
Gln	Gln	Cys	Glu	Ala	Lys	Cys	Asp	Ser	Pro	Thr	Pro	Gly	Asp	Gly	Pro		
1025					1030					1035					1040		
Glu	Glu	Cys	Lys	Asp	Val	Asn	Lys	Val	Ala	Tyr	Cys	Pro	Leu	Val	Leu		

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Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys		
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Thr Cys Gln Gly His		
1075		
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<213> Homo sapiens		
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Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala		
20 25 30		
Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro		
35 40 45		
Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro		
50 55 60		
Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala		
65 70 75 80		
Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr		
85 90 95		
Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg		
100 105 110		
Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys		
115 120 125		
His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala		
130 135 140		
Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn		
145 150 155 160		
Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly		
165 170 175		
His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala Pro Glu Arg Leu		
180 185 190		
Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys Gly Val Gln Val		
195 200 205		
Tyr Pro Glu Leu Glu Ser Arg Arg Glu Arg Trp Glu Gln Arg Gln Gln		
210 215 220		



Trp	Arg	Arg	Pro	Arg	Leu	Arg	Arg	Leu	His	Gln	Arg	Ser	Val	Ser	Lys	225	230	235	240
Glu	Lys	Trp	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Ala	Lys	Met	Val	Glu	245	250	255	
Tyr	His	Gly	Gln	Pro	Gln	Val	Glu	Ser	Tyr	Val	Leu	Thr	Ile	Met	Asn	260	265	270	
Met	Val	Ala	Gly	Leu	Phe	His	Asp	Pro	Ser	Ile	Gly	Asn	Pro	Ile	His	275	280	285	
Ile	Thr	Ile	Val	Arg	Leu	Val	Leu	Leu	Glu	Asp	Glu	Glu	Glu	Asp	Leu	290	295	300	
Lys	Ile	Thr	His	His	Ala	Asp	Asn	Thr	Leu	Lys	Ser	Phe	Cys	Lys	Trp	305	310	315	320
Gln	Lys	Ser	Ile	Asn	Met	Lys	Gly	Asp	Ala	His	Pro	Leu	His	His	Asp	325	330	335	
Thr	Ala	Ile	Leu	Leu	Thr	Arg	Lys	Asp	Leu	Cys	Ala	Ala	Met	Asn	Arg	340	345	350	
Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Val	Ala	Gly	Met	Cys	Gln	Pro	355	360	365	
His	Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Pro	Leu	Ala	Phe	370	375	380	
Thr	Val	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	Gln	His	Asp	Gly	385	390	395	400
Ser	Gly	Asn	Asp	Cys	Glu	Pro	Val	Gly	Lys	Arg	Pro	Phe	Ile	Met	Ser	405	410	415	
Pro	Gln	Leu	Leu	Tyr	Asp	Ala	Ala	Pro	Leu	Thr	Trp	Ser	Arg	Cys	Ser	420	425	430	
Arg	Gln	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	Gly	Leu	Cys	Leu	435	440	445	
Asp	Asp	Pro	Pro	Ala	Lys	Asp	Ile	Ile	Asp	Phe	Pro	Ser	Val	Pro	Pro	450	455	460	
Gly	Val	Leu	Tyr	Asp	Val	Ser	His	Gln	Cys	Arg	Leu	Gln	Tyr	Gly	Ala	465	470	475	480
Tyr	Ser	Ala	Phe	Cys	Glu	Asp	Met	Asp	Asn	Val	Cys	His	Thr	Leu	Trp	485	490	495	
Cys	Ser	Val	Gly	Thr	Thr	Cys	His	Ser	Lys	Leu	Asp	Ala	Ala	Val	Asp	500	505	510	
Gly	Thr	Arg	Cys	Gly	Glu	Asn	Lys	Trp	Cys	Leu	Ser	Gly	Glu	Cys	Val	515	520	525	

Pro Val Gly Phe Arg Pro Glu Ala Val Asp Gly Gly Trp Ser Gly Trp  
 530 535 540  
 Ser Ala Trp Ser Ile Cys Ser Arg Ser Cys Gly Met Gly Val Gln Ser  
 545 550 555 560  
 Ala Glu Arg Gln Cys Thr Gln Pro Thr Pro Lys Tyr Lys Gly Arg Tyr  
 565 570 575  
 Cys Val Gly Glu Arg Lys Arg Phe Arg Leu Cys Asn Leu Gln Ala Cys  
 580 585 590  
 Pro Ala Gly Arg Pro Ser Phe Arg His Val Gln Cys Ser His Phe Asp  
 595 600 605  
 Ala Met Leu Tyr Lys Gly Gln Leu His Thr Trp Val Pro Val Val Asn  
 610 615 620  
 Asp Val Asn Pro Cys Glu Leu His Cys Arg Pro Ala Asn Glu Tyr Phe  
 625 630 635 640  
 Ala Lys Lys Leu Arg Asp Ala Val Val Asp Gly Thr Pro Cys Tyr Gln  
 645 650 655  
 Val Arg Ala Ser Arg Asp Leu Cys Ile Asn Gly Ile Cys Lys Asn Val  
 660 665 670  
 Gly Cys Asp Phe Glu Ile Asp Ser Gly Ala Met Glu Asp Arg Cys Gly  
 675 680 685  
 Val Cys His Gly Asn Gly Ser Thr Cys His Thr Val Ser Gly Thr Phe  
 690 695 700  
 Glu Glu Ala Glu Gly Leu Gly Tyr Val Asp Val Gly Leu Ile Pro Ala  
 705 710 715 720  
 Gly Ala Arg Glu Ile Arg Ile Gln Glu Val Ala Glu Ala Ala Asn Phe  
 725 730 735  
 Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe Leu Asn Gly Gly  
 740 745 750  
 Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala Gly Thr Thr Phe  
 755 760 765  
 Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr Ser Pro Gly Pro  
 770 775 780  
 Thr Lys Glu Pro Val Trp Ile Gln Val Pro Ala Ser Arg Gly Pro Gly  
 785 790 795 800  
 Gly Gly Ser Arg Gly Gly Val Pro Arg Pro Ser Thr Leu His Gly Arg  
 805 810 815  
 Ser Arg Pro Gly Gly Val Ser Pro Gly Ser Val Thr Glu Pro Gly Ser  
 820 825 830

Glu Pro Gly Pro Pro Ala Ala Ala Ser Thr Ser Val Ser Pro Ser Leu  
 835 840 845  
 Lys Trp Pro Asn Leu Val Ala Ala Val His Arg Gly Gly Trp Gly Gln  
 850 855 860  
 Ala Pro Leu Gly Leu Gly Gly Trp Arg Arg His Leu Val Leu Met Gly  
 865 870 875 880  
 Pro Arg Leu Pro Thr Gln Leu Leu Phe Gln Glu Ser Asn Pro Gly Val  
 885 890 895  
 His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly His Asp Glu Val  
 900 905 910  
 Pro Pro Pro Val Phe Ser Trp His Tyr Gly Pro Trp Thr Lys Cys Thr  
 915 920 925  
 Val Thr Cys Gly Arg Gly Glu Lys Trp Gly Arg His Ser Pro Thr Cys  
 930 935 940  
 Arg Gly Leu Val Ser Gly Gln Gly His Trp Leu Gln Leu Pro Ala His  
 945 950 955 960  
 Cys Trp Ala Thr Thr Gly Leu Glu Val Cys Phe Ser Glu Pro Gln Phe  
 965 970 975  
 Ser Ile Cys Glu Met Arg Leu Ala Ile Ala Leu Cys Pro Arg Pro Ala  
 980 985 990  
 Gly Arg Val His Gly  
 995

<210> 33  
 <211> 854  
 <212> PRT  
 <213> Homo sapiens

<400> 33  
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 1 5 10 15  
 Ala Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly  
 20 25 30  
 Ser Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp  
 35 40 45  
 Gln Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser  
 50 55 60  
 Phe Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn  
 65 70 75 80  
 Ala Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile  
 85 90 95

Thr	Arg	Tyr	Asp	Ile	Cys	Ile	Tyr	Lys	Asn	Lys	Pro	Cys	Gly	Thr	Leu	
			100					105					110			
Gly	Leu	Ala	Pro	Val	Gly	Gly	Met	Cys	Glu	Arg	Glu	Arg	Ser	Cys	Ser	
		115					120					125				
Val	Asn	Glu	Asp	Ile	Gly	Leu	Ala	Thr	Ala	Phe	Thr	Ile	Ala	His	Glu	
	130					135					140					
Ile	Gly	His	Thr	Phe	Gly	Met	Asn	His	Asp	Gly	Val	Gly	Asn	Ser	Cys	
145					150					155					160	
Gly	Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	
				165					170					175		
Met	Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Ser	Arg	Asp	Tyr	Ile	
			180					185					190			
Thr	Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	
		195					200					205				
Pro	Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	
	210					215					220					
Asp	Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	
225					230					235					240	
Cys	Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	
				245					250					255		
Asn	Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	
			260					265					270			
Gln	Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	
		275					280					285				
Pro	Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	
	290					295					300					
Thr	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	
305					310					315					320	
Ser	Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	
				325				330						335		
Cys	Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	
			340					345					350			
Pro	Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	
		355					360					365				
Ser	Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	
	370					375					380					
Gly	Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Cys	Leu	Ala	Glu	Gly	Phe	Asn	
385					390					395					400	

Phe Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg  
405 410 415  
Pro Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly  
420 425 430  
Cys Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val  
435 440 445  
Cys Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser  
450 455 460  
Pro Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys  
465 470 475 480  
Gly Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His  
485 490 495  
Leu Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro  
500 505 510  
Gly Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln  
515 520 525  
Leu Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro  
530 535 540  
Ile Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro  
545 550 555 560  
Ala Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro  
565 570 575  
Pro Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys  
580 585 590  
Ala Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp  
595 600 605  
Ser Ser Ala Val Ala Pro His Tyr Cys Ser Ala His Ser Lys Leu Pro  
610 615 620  
Lys Arg Gln Arg Ala Cys Asn Thr Glu Pro Cys Pro Pro Asp Trp Val  
625 630 635 640  
Val Gly Asn Trp Ser Leu Cys Ser Arg Ser Cys Asp Ala Gly Val Arg  
645 650 655  
Ser Arg Ser Val Val Cys Gln Arg Arg Val Ser Ala Ala Glu Glu Lys  
660 665 670  
Ala Leu Asp Asp Ser Ala Cys Pro Gln Pro Arg Pro Pro Val Leu Glu  
675 680 685  
Ala Cys His Gly Pro Thr Cys Pro Pro Glu Trp Ala Ala Leu Asp Trp  
690 695 700

Ser Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val  
 705 710 715 720  
 Leu Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys  
 725 730 735  
 Ser Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg  
 740 745 750  
 Cys Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala  
 755 760 765  
 Gln Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His  
 770 775 780  
 Thr Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr  
 785 790 795 800  
 Thr Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly  
 805 810 815  
 Pro Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val  
 820 825 830  
 Leu Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys  
 835 840 845  
 Lys Thr Cys His Gly His  
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<210> 34  
 <211> 860  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (450)  
 <223> Wherein Xaa is any amino acid.

<400> 34  
 Met Glu Ile Leu Trp Lys Thr Leu Thr Trp Ile Leu Ser Leu Ile Met  
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 Ala Ser Ser Glu Phe His Ser Asp His Arg Leu Ser Tyr Ser Ser Gln  
 20 25 30  
 Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile  
 35 40 45  
 Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp  
 50 55 60  
 Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln  
 65 70 75 80

Ala	Val	Ser	Lys	Leu	Phe	Phe	Lys	Leu	Ser	Ala	Tyr	Gly	Lys	His	Phe	
				85					90					95		
His	Leu	Asn	Leu	Thr	Leu	Asn	Thr	Asp	Phe	Val	Ser	Lys	His	Phe	Thr	
			100					105					110			
Val	Glu	Tyr	Trp	Gly	Lys	Asp	Gly	Pro	Gln	Trp	Lys	His	Asp	Phe	Leu	
		115					120					125				
Asp	Asn	Cys	His	Tyr	Thr	Gly	Tyr	Leu	Gln	Asp	Gln	Arg	Ser	Thr	Thr	
	130					135					140					
Lys	Val	Ala	Leu	Ser	Asn	Cys	Val	Gly	Leu	His	Gly	Val	Ile	Ala	Thr	
145					150					155					160	
Glu	Asp	Glu	Glu	Tyr	Phe	Ile	Glu	Pro	Leu	Lys	Asn	Thr	Thr	Glu	Asp	
				165					170					175		
Ser	Lys	His	Phe	Ser	Tyr	Glu	Asn	Gly	His	Pro	His	Val	Ile	Tyr	Lys	
			180					185					190			
Lys	Ser	Ala	Leu	Gln	Gln	Arg	His	Leu	Tyr	Asp	His	Ser	His	Cys	Gly	
		195					200					205				
Val	Ser	Asp	Phe	Thr	Arg	Ser	Gly	Lys	Pro	Trp	Trp	Leu	Asn	Asp	Thr	
	210					215					220					
Ser	Thr	Val	Ser	Tyr	Ser	Leu	Pro	Ile	Asn	Asn	Thr	His	Ile	His	His	
225					230					235					240	
Arg	Gln	Lys	Arg	Ser	Val	Ser	Ile	Glu	Arg	Phe	Val	Glu	Thr	Leu	Val	
				245					250					255		
Val	Ala	Asp	Lys	Met	Met	Val	Gly	Tyr	His	Gly	Arg	Lys	Asp	Ile	Glu	
			260					265					270			
His	Tyr	Ile	Leu	Ser	Val	Met	Asn	Ile	Val	Ala	Lys	Leu	Tyr	Arg	Asp	
		275					280					285				
Ser	Ser	Leu	Gly	Asn	Val	Val	Asn	Ile	Ile	Val	Ala	Arg	Leu	Ile	Val	
	290					295					300					
Leu	Thr	Glu	Asp	Gln	Pro	Asn	Leu	Glu	Ile	Asn	His	His	Ala	Asp	Lys	
305					310					315					320	
Ser	Leu	Asp	Ser	Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Leu	Ser	His	Gln	
				325					330					335		
Ser	Asp	Gly	Asn	Thr	Ile	Pro	Glu	Asn	Gly	Ile	Ala	His	His	Asp	Asn	
			340					345					350			
Ala	Val	Leu	Ile	Thr	Arg	Tyr	Asp	Ile	Cys	Thr	Tyr	Lys	Asn	Lys	Pro	
		355					360					365				
Cys	Gly	Thr	Leu	Gly	Leu	Ala	Ser	Val	Ala	Gly	Met	Cys	Glu	Pro	Glu	
	370					375					380					

Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Ile	Gly	Leu	Gly	Ser	Ala	Phe	Thr	385	390	395	400
Ile	Ala	His	Glu	Ile	Val	His	Asn	Phe	Gly	Met	Asn	His	Asp	Gly	Ile	405	410	415	
Gly	Asn	Ser	Cys	Gly	Arg	Lys	Val	Met	Lys	Gln	Gln	Asn	Tyr	Gly	Ser	420	425	430	
Ser	His	Tyr	Cys	Glu	Tyr	Gln	Ser	Phe	Phe	Leu	Val	Cys	Leu	Gln	Ser	435	440	445	
Arg	Xaa	His	His	Gln	Leu	Phe	Arg	Glu	Val	Cys	Arg	Glu	Leu	Trp	Cys	450	455	460	
Leu	Ser	Lys	Ser	Asn	Arg	Cys	Val	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	465	470	475	480
Gly	Thr	Leu	Cys	Gln	Thr	Gly	Asn	Ile	Glu	Lys	Gly	Trp	Cys	Tyr	Gln	485	490	495	
Gly	Asp	Cys	Val	Pro	Phe	Gly	Thr	Trp	Pro	Gln	Ser	Ile	Asp	Gly	Gly	500	505	510	
Trp	Gly	Pro	Trp	Ser	Leu	Trp	Gly	Glu	Cys	Ser	Arg	Thr	Cys	Gly	Gly	515	520	525	
Gly	Val	Ser	Ser	Ser	Leu	Arg	His	Cys	Asp	Ser	Pro	Ala	Pro	Ser	Gly	530	535	540	
Gly	Gly	Lys	Tyr	Cys	Leu	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Ser	Cys	Asn	545	550	555	560
Thr	Asp	Pro	Cys	Pro	Leu	Gly	Ser	Arg	Asp	Phe	Arg	Glu	Lys	Gln	Cys	565	570	575	
Ala	Asp	Phe	Asp	Asn	Met	Pro	Phe	Arg	Gly	Lys	Tyr	Tyr	Asn	Trp	Lys	580	585	590	
Pro	Tyr	Thr	Gly	Gly	Gly	Val	Lys	Pro	Cys	Ala	Leu	Asn	Cys	Leu	Ala	595	600	605	
Glu	Gly	Tyr	Asn	Phe	Tyr	Thr	Glu	Arg	Ala	Pro	Ala	Val	Ile	Asp	Gly	610	615	620	
Thr	Gln	Cys	Asn	Ala	Asp	Ser	Leu	Asp	Ile	Cys	Ile	Asn	Gly	Glu	Cys	625	630	635	640
Lys	His	Val	Gly	Cys	Asp	Asn	Ile	Leu	Gly	Ser	Asp	Ala	Arg	Glu	Asp	645	650	655	
Arg	Cys	Arg	Val	Cys	Gly	Gly	Gly	Gly	Ser	Thr	Cys	Asp	Ala	Ile	Glu	660	665	670	
Gly	Phe	Phe	Asn	Asp	Ser	Leu	Pro	Arg	Gly	Gly	Tyr	Met	Glu	Val	Val	675	680	685	



Gln Ile Pro Arg Gly Ser Val His Ile Glu Val Arg Glu Val Ala Met  
 690 695 700  
 Ser Lys Asn Tyr Ile Ala Leu Lys Ser Glu Gly Asp Asp Tyr Tyr Ile  
 705 710 715 720  
 Asn Gly Ala Trp Thr Ile Asp Trp Pro Arg Lys Phe Asp Val Ala Gly  
 725 730 735  
 Thr Ala Phe His Tyr Lys Arg Pro Thr Asp Glu Pro Glu Ser Leu Glu  
 740 745 750  
 Ala Leu Gly Pro Thr Ser Glu Asn Leu Ile Val Met Val Leu Leu Gln  
 755 760 765  
 Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg  
 770 775 780  
 Thr Gly Ser Gly Asp Asn Glu Val Gly Phe Thr Trp Asn His Gln Pro  
 785 790 795 800  
 Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Lys Met Pro Thr Arg  
 805 810 815  
 Gln Pro Thr Gln Arg Ala Arg Trp Arg Thr Lys His Ile Leu Ser Tyr  
 820 825 830  
 Ala Leu Cys Leu Leu Lys Lys Leu Ile Gly Asn Ile Ser Cys Arg Phe  
 835 840 845  
 Ala Ser Ser Cys Asn Leu Ala Lys Glu Thr Leu Leu  
 850 855 860

<210> 35  
 <211> 936  
 <212> PRT  
 <213> Homo sapiens

<400> 35  
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 Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu  
 20 25 30  
 Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg  
 35 40 45  
 Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln  
 50 55 60  
 Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val  
 65 70 75 80  
 Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu

85								90				95			
Asn	Asp	Gln	Asp	Asn	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile
		100						105					110		
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met
		115					120					125			
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys
	130					135					140				
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His
145					150					155					160
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly
				165					170					175	
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr
			180					185					190		
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val
		195					200					205			
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile
		210				215					220				
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu
225					230					235					240
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
				245					250					255	
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260					265					270		
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
		275					280					285			
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu
		290				295					300				
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp
305					310					315					320
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala
				325					330					335	
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val
			340					345					350		
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu
		355					360					365			
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro
		370				375					380				
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn

385		390		395		400
Val Val Glu Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile						
		405		410		415
Leu Gly Ser Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr						
		420		425		430
Gly Cys Gly Glu Gln Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val						
		435		440		445
Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser						
		450		455		460
Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr						
		465		470		475
Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg						
		485		490		495
Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala						
		500		505		510
Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala						
		515		520		525
Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser						
		530		535		540
Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu						
		545		550		555
Val Thr Leu Ser Ala Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu						
		565		570		575
Thr Val Thr His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser						
		580		585		590
Ala Trp Lys Thr Ala Gln Glu Gly Asp His Gly Ser His Val Tyr Thr						
		595		600		605
Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys						
		610		615		620
Arg Lys Glu Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp						
		625		630		635
Asn Ser Val His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly						
		645		650		655
His Phe Tyr Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser						
		660		665		670
Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu						
		675		680		685
Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln						

690					695					700					
Asn	Ala	Gln	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu
705					710					715					720
His	Ala	Leu	Ser	Lys	Tyr	Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys
				725					730					735	
Ala	Ala	Gln	Val	Thr	Ile	Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe
			740						745					750	
Gln	Val	Asp	Asn	Asn	Asn	Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro
		755					760					765			
Glu	Leu	Pro	Gly	Glu	Tyr	Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val
	770					775					780				
Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu
785					790					795					800
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu
				805					810					815	
Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr
			820					825						830	
Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val
		835					840					845			
Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser
	850					855					860				
Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr
865					870					875					880
Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu
				885					890					895	
Gln	Asp	Val	Pro	Val	Arg	Asp	Leu	Lys	Pro	Ala	Ile	Val	Lys	Val	Tyr
			900					905						910	
Asp	Tyr	Tyr	Glu	Thr	Gly	Glu	Phe	Ala	Ile	Ala	Glu	Tyr	Asn	Ala	Pro
		915					920					925			
Cys	Ser	Lys	Asp	Leu	Gly	Asn	Ala								
	930					935									

<210> 36

<211> 898

<212> PRT

<213> Homo sapiens

<400> 36

Arg	Leu	Leu	Ile	Tyr	Ala	Val	Leu	Pro	Thr	Gly	Asp	Val	Ile	Gly	Asp
1				5					10					15	

Ser	Ala	Lys	Tyr	Asp	Val	Glu	Asn	Cys	Leu	Ala	Asn	Lys	Val	Asp	Leu	20	25	30	
Ser	Phe	Ser	Pro	Ser	Gln	Ser	Leu	Pro	Ala	Ser	His	Ala	His	Leu	Arg	35	40	45	
Val	Thr	Ala	Ala	Pro	Gln	Ser	Val	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln	50	55	60	
Ser	Val	Leu	Leu	Met	Lys	Pro	Asp	Ala	Glu	Leu	Ser	Ala	Ser	Ser	Val	65	70	75	80
Tyr	Asn	Leu	Leu	Pro	Glu	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Pro	Leu	85	90	95	
Asn	Asp	Gln	Asp	Asp	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile	100	105	110	
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met	115	120	125	
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys	130	135	140	
Ile	Arg	Lys	Glu	Glu	Pro	His	Thr	Glu	Thr	Val	Arg	Lys	Tyr	Phe	Pro	145	150	155	160
Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	Asn	Ser	Ala	Gly	Val	Ala	165	170	175	
Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	180	185	190	
Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	Gly	Ile	Ser	Ser	Thr	Ala	195	200	205	
Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	210	215	220	
Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	225	230	235	240
Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val	Gln	Leu	Glu	Ala	Ser	Pro	245	250	255	
Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu	Gln	Ala	Pro	His	Cys	Ile	260	265	270	
Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp	Ala	Val	Thr	Pro	Lys	Ser	275	280	285	
Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Gln	290	295	300	
Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val	Pro	Glu	His	Gly	Arg	Lys	305	310	315	320

Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu	Lys	325	330	335	
Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Ser	Gly	Gly	Glu	Val	Ser	340	345	350	
Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	Val	Val	Glu	Glu	Ser	Ala	355	360	365	
Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	370	375	380	
Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	385	390	395	400
Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu	405	410	415	
Thr	Gln	Gln	Leu	Thr	Pro	Glu	Val	Lys	Ser	Lys	Ala	Ile	Gly	Tyr	Leu	420	425	430	
Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Tyr	Asp	Gly	Ser	435	440	445	
Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg	Asn	Gln	Gly	Asn	Thr	Trp	450	455	460	
Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala	Gln	Ala	Arg	Ala	Tyr	Ile	465	470	475	480
Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala	Leu	Ile	Trp	Leu	Ser	Gln	485	490	495	
Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu	Asn	500	505	510	
Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala	Tyr	515	520	525	
Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu	Thr	Val	Thr	His	Pro	Val	530	535	540	
Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser	Ala	Trp	Lys	Thr	Ala	Gln	545	550	555	560
Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	565	570	575	
Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys	Arg	Lys	Glu	Val	Leu	Lys	580	585	590	
Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp	Asn	Ser	Val	His	Trp	Glu	595	600	605	
Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly	His	Phe	Tyr	Glu	Pro	Gln	610	615	620	

Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser	Tyr	Val	Leu	Leu	Ala	Tyr	625	630	635	640
Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu	Asp	Leu	Thr	Ser	Ala	Thr	645	650	655	
Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln	Asn	Ala	Gln	Gly	Gly	Phe	660	665	670	
Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	Tyr	675	680	685	
Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys	Ala	Ala	Gln	Val	Thr	Ile	690	695	700	
Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe	Gln	Val	Asp	Asn	Asn	Asn	705	710	715	720
Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro	Glu	Leu	Pro	Gly	Glu	Tyr	725	730	735	
Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser	Leu	740	745	750	
Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu	Phe	Pro	Phe	Ala	Leu	Gly	755	760	765	
Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu	Pro	Lys	Ala	His	Thr	Ser	770	775	780	
Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Ala	Ser	785	790	795	800
Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro	Leu	805	810	815	
Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	Asn	His	Val	Ser	Arg	Thr	820	825	830	
Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	Asn	835	840	845	
Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu	Gln	Asp	Val	Pro	Val	Arg	850	855	860	
Asp	Leu	Lys	Pro	Ala	Ile	Val	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Thr	Asp	865	870	875	880
Glu	Phe	Ala	Ile	Ala	Glu	Tyr	Asn	Ala	Pro	Cys	Ser	Lys	Asp	Leu	Gly	885	890	895	
Asn	Ala																		

<210> 37  
<211> 936

<212> PRT  
 <213> Homo sapiens

<400> 37

Arg	Leu	Leu	Ile	Tyr	Ala	Val	Leu	Pro	Thr	Gly	Asp	Val	Ile	Gly	Asp
1				5					10					15	
Ser	Ala	Lys	Tyr	Asp	Val	Glu	Asn	Glu	Leu	Ala	Asn	Lys	Val	Asp	Leu
			20				25						30		
Ser	Phe	Ser	Pro	Ser	Gln	Ser	Leu	Pro	Ala	Ser	His	Ala	His	Leu	Arg
		35					40					45			
Val	Thr	Ala	Ala	Pro	Gln	Ser	Val	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln
	50					55					60				
Ser	Val	Leu	Leu	Met	Lys	Pro	Asp	Ala	Glu	Leu	Ser	Ala	Ser	Ser	Val
65					70					75					80
Tyr	Asn	Leu	Leu	Pro	Glu	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Pro	Leu
				85					90					95	
Asn	Asp	Gln	Asp	Asp	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile
		100						105					110		
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met
		115					120					125			
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys
	130					135					140				
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His
145					150					155					160
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly
			165						170					175	
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr
			180					185					190		
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val
		195					200					205			
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile
	210					215					220				
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu
225					230					235					240
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
				245					250					255	
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260					265					270		
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
		275					280					285			



Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu			
290						295					300							
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp			
305					310					315					320			
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala			
				325					330					335				
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val			
			340					345					350					
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu			
		355					360					365						
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro			
		370				375					380							
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn			
385					390					395					400			
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile			
				405					410					415				
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr			
			420					425					430					
Gly	Cys	Gly	Glu	Glx	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val			
		435					440					445						
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser			
	450					455					460							
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr			
465					470					475					480			
Lys	His	Tyr	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg			
			485						490					495				
Asn	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala			
			500					505					510					
Gln	Ala	Arg	Ala	Tyr	Ile	Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala			
		515					520					525						
Leu	Ile	Trp	Leu	Ser	Gln	Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser			
	530					535					540							
Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu			
545					550					555					560			
Val	Thr	Leu	Ser	Ala	Tyr	Ile	Lys	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu			
				565					570					575				
Thr	Val	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser			
			580					585					590					

Ala	Trp	Lys	Thr	Ala	Glu	Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr		
		595					600					605					
Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys		
	610					615					620						
Arg	Lys	Glu	Val	Leu	Lys	Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp		
625					630					635					640		
Asn	Ser	Val	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly		
				645					650					655			
His	Phe	Tyr	Glu	Pro	Gln	Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser		
			660					665					670				
Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu		
		675					680					685					
Asp	Leu	Thr	Ser	Ala	Thr	Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln		
	690					695					700						
Asn	Ala	Gln	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Lys	Val	Val	Ala	Leu		
705					710					715					720		
His	Ala	Leu	Ser	Lys	Tyr	Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys		
				725					730					735			
Ala	Ala	Gln	Val	Thr	Ile	Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe		
			740					745					750				
Gln	Val	Asp	Asn	Asn	Asn	Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro		
		755					760					765					
Glu	Leu	Pro	Gly	Glu	Tyr	Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val		
	770					775					780						
Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu		
785					790					795					800		
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu		
				805					810					815			
Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr		
			820					825					830				
Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val		
		835					840					845					
Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser		
	850					855					860						
Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr		
865					870					875					880		
Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu		
				885				890						895			

Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr  
 900 905 910

Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro  
 915 920 925

Cys Ser Lys Asp Leu Gly Asn Ala  
 930 935

<210> 38

<211> 931

<212> PRT

<213> Rattus norvegicus

<400> 38

Arg Leu Val Leu Tyr Ala Ile Leu Pro Asn Gly Glu Val Val Gly Asp  
 1 5 10 15

Thr Ala Lys Tyr Glu Ile Glu Asn Cys Leu Ala Asn Lys Val Asp Leu  
 20 25 30

Val Phe Arg Pro Asn Ser Gly Leu Pro Ala Thr Arg Ala Leu Leu Ser  
 35 40 45

Val Met Ala Ser Pro Gln Ser Leu Cys Gly Leu Arg Ala Val Asp Gln  
 50 55 60

Ser Val Leu Leu Met Lys Pro Glu Thr Glu Leu Ser Ala Ser Leu Ile  
 65 70 75 80

Tyr Asp Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gln Gly Ala  
 85 90 95

Asp Gln Arg Glu Glu Asp Thr Asn Gly Cys Val Lys Gln Asn Asp Thr  
 100 105 110

Tyr Ile Asn Gly Ile Leu Tyr Ser Pro Val Gln Asn Thr Asn Glu Glu  
 115 120 125

Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn  
 130 135 140

Ser Asn Ile Arg Lys Pro Lys Val Cys Glu Arg Leu Arg Asp Asn Lys  
 145 150 155 160

Gly Ile Pro Ala Ala Tyr His Leu Val Ser Gln Ser His Met Asp Ala  
 165 170 175

Phe Leu Glu Ser Ser Glu Ser Pro Thr Glu Thr Arg Arg Ser Tyr Phe  
 180 185 190

Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val Asp Ser Ala Gly Val  
 195 200 205

Ala Glu Val Glu Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala

210					215					220					
Gly	Ala	Phe	Cys	Leu	Ser	Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Val
225					230					235					240
Val	Gln	Phe	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro
				245					250					255	
Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu
			260					265					270		
Asn	Tyr	Leu	Pro	Thr	Cys	Ile	Arg	Val	Ala	Val	Gln	Leu	Glu	Ala	Ser
		275					280					285			
Pro	Asp	Phe	Leu	Ala	Ala	Pro	Glu	Glu	Lys	Glu	Gln	Arg	Ser	His	Cys
	290					295					300				
Ile	Cys	Met	Asn	Gln	Arg	His	Thr	Ala	Ser	Trp	Ala	Val	Ile	Pro	Lys
305				310						315				320	
Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Asn	Ser
			325					330						335	
Lys	Glu	Leu	Cys	Gly	Asn	Glu	Val	Pro	Val	Val	Pro	Glu	Gln	Gly	Lys
			340					345					350		
Lys	Asp	Thr	Ile	Ile	Lys	Ser	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu
	355						360					365			
Asn	Glu	Val	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Met	Gly	Ala	Glu	Val
	370					375					380				
Ser	Glu	Leu	Ile	Ala	Leu	Lys	Leu	Pro	Ser	Asp	Val	Val	Glu	Glu	Ser
385				390						395				400	
Ala	Arg	Ala	Ser	Val	Thr	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met
			405					410						415	
Gln	Asn	Thr	Gln	Asp	Leu	Leu	Lys	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln
			420				425						430		
Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn
		435					440					445			
Glu	Thr	Gln	Gln	Leu	Thr	Gln	Glu	Ile	Lys	Thr	Lys	Ala	Ile	Ala	Tyr
	450					455					460				
Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly
465				470					475					480	
Ser	Tyr	Ser	Ala	Phe	Gly	Asp	Lys	Pro	Gly	Arg	Asn	His	Ala	Asn	Thr
			485					490					495		
Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Lys	Tyr
			500				505						510		
Ile	Phe	Ile	Asp	Glu	Val	His	Ile	Thr	Gln	Ala	Leu	Leu	Trp	Leu	Ser

515					520					525					
Gln	Gln	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu
530						535					540				
Asn	Asn	Ala	Met	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala
545					550					555					560
Tyr	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Met	Ser	Leu	Pro	Val	Thr	His	Pro
				565					570					575	
Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala
			580						585				590		
Arg	Gly	Gly	Ala	Gly	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala
		595					600					605			
Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys
	610					615					620				
Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala	Arg	Gly	Gly	Ala	Gly	Gly	Ser	His
625					630					635					640
Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro
				645					650					655	
Gln	Ala	Thr	Ser	Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Val	Leu	Leu	Ala
			660					665					670		
Tyr	Leu	Thr	Thr	Glu	Pro	Ala	Pro	Thr	Gln	Glu	Asp	Leu	Thr	Ala	Ala
		675					680					685			
Met	Leu	Ile	Val	Lys	Trp	Leu	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly
	690					695					700				
Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys
705					710					715					720
Tyr	Gly	Ser	Ala	Thr	Phe	Thr	Arg	Ala	Lys	Lys	Ala	Ala	Gln	Val	Thr
				725					730					735	
Ile	Arg	Ser	Ser	Gly	Thr	Phe	Ser	Thr	Lys	Phe	Gln	Val	Asn	Asn	Asn
			740					745					750		
Asn	Gln	Leu	Leu	Leu	Gln	Arg	Val	Thr	Leu	Pro	Thr	Val	Pro	Gly	Asp
		755					760					765			
Tyr	Thr	Val	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser
	770					775					780				
Leu	Lys	Tyr	Ser	Val	Leu	Pro	Arg	Glu	Glu	Glu	Phe	Pro	Phe	Ala	Val
785					790					795					800
Val	Val	Gln	Thr	Leu	Pro	Gly	Thr	Cys	Glu	Asp	Pro	Lys	Ala	His	Thr
				805					810					815	
Ser	Phe	Gln	Ile	Ser	Leu	Asn	Ile	Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Glu

	820		825		830										
Ser	Asn	Met	Ala	Ile	Ala	Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro
	835						840					845			
Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	Val	His	Val	Ser	Arg
	850					855					860				
Thr	Glu	Val	Ser	Asn	Asn	His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser
865					870					875					880
Asn	Gln	Thr	Val	Asn	Leu	Ser	Phe	Thr	Val	Gln	Gln	Asp	Ile	Pro	Ile
				885					890					895	
Arg	Asp	Leu	Lys	Pro	Ala	Val	Val	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Lys
			900					905					910		
Asp	Glu	Phe	Ala	Val	Ala	Lys	Tyr	Ser	Ala	Pro	Cys	Ser	Thr	Asp	Tyr
	915						920					925			
Gly	Asn	Ala													
	930														

<210> 39  
 <211> 941  
 <212> PRT  
 <213> Cavia porcellus

<400> 39  
 Arg Val Leu Ile Tyr Ala Ile Leu Pro Ser Gly Glu Ile Ile Ala Asp  
 1 5 10 15  
 Ser Ala Lys Tyr Asn Val Glu Asn Cys Leu Asp Asn Lys Val Asn Leu  
 20 25 30  
 Ser Phe Ser Glu Gly Gln Ser Leu Pro Ala Ser Lys Thr His Leu Arg  
 35 40 45  
 Val Thr Ala Ser Pro Gln Ser Leu Cys Ala Leu Arg Ala Val Asp Gln  
 50 55 60  
 Ser Val Leu Leu Arg Lys Pro Glu Ala Val Leu Ser Ala Ser Ser Val  
 65 70 75 80  
 Tyr Ala Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gly Leu Leu  
 85 90 95  
 Gly Gln Gln Glu Glu Asn Asp Gly Glu Cys Val Ser Leu Tyr Asn Thr  
 100 105 110  
 Tyr Ile Asp Gly Ile Leu Tyr Ser Pro Glu Pro Asn Ile Asn Glu Lys  
 115 120 125  
 Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn  
 130 135 140

Thr	Lys	Ile	Gln	Lys	Pro	Gln	Leu	Cys	Ala	His	Val	Gln	Lys	Phe	Glu	145	150	155	160
Val	Pro	Thr	Met	Ala	Tyr	Ser	Tyr	Ser	Glu	Ser	Ser	Ser	Phe	Arg	Ser	165	170	175	
Gly	Pro	Arg	Arg	Val	Pro	Ala	Val	Gly	Ile	Ala	Ala	Thr	Tyr	Ser	Glu	180	185	190	
Pro	Pro	Lys	Glu	Thr	Val	Arg	Thr	Tyr	Ser	Pro	Glu	Thr	Trp	Ile	Trp	195	200	205	
Asp	Leu	Lys	Val	Thr	Asp	Ser	Ser	Gly	Val	Ala	Glu	Val	Glu	Val	Thr	210	215	220	
Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	225	230	235	240
Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Thr	Ala	Ser	Leu	Arg	Ala	Phe	245	250	255	
Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	260	265	270	
Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Asp	Cys	275	280	285	
Ile	Arg	Ile	Ser	Val	His	Leu	Glu	Ala	Ser	Pro	Lys	Phe	Leu	Ala	Glu	290	295	300	
Pro	Lys	Ala	Lys	Glu	Gln	Glu	Ser	Tyr	Cys	Val	Cys	Gly	Asn	Glu	Arg	305	310	315	320
Gln	Thr	Val	Ser	Trp	Val	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	325	330	335	
Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Ser	Glu	Leu	Cys	Gly	Asn	340	345	350	
Glu	Lys	Thr	Val	Val	Pro	Thr	Tyr	Gly	Lys	Lys	Asp	Thr	Ile	Ile	Lys	355	360	365	
Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Ile	Glu	Lys	Glu	Glu	Thr	Trp	Thr	370	375	380	
Ser	Leu	Ile	Arg	Val	Ser	Asp	Thr	Thr	Val	Ser	Glu	Lys	Leu	His	Leu	385	390	395	400
Glu	Leu	Pro	Ser	Asn	Val	Ile	Gln	Asp	Ser	Ala	Arg	Ala	Thr	Val	Ser	405	410	415	
Ile	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	Asn	Ile	Gln	Asn	Leu	420	425	430	
Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala	435	440	445	

Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr		
	450					455					460						
Pro	Asp	Ile	Lys	Ser	Lys	Ala	Ile	Ser	Tyr	Leu	Ser	Thr	Gly	Tyr	Gln		
465					470					475					480		
Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly		
				485					490					495			
Glu	Asn	Tyr	Arg	Gly	Gly	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val		
			500					505					510				
Leu	Lys	Thr	Phe	Ser	Gln	Ala	Arg	Lys	Tyr	Ile	Phe	Ile	Asp	Glu	Ala		
		515					520					525					
His	Ile	Thr	Gln	Ala	Leu	Ser	Trp	Leu	Ser	Gln	Lys	Gln	Lys	Asp	Asn		
	530					535					540						
Gly	Cys	Phe	Trp	Ser	Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly		
545					550					555					560		
Gly	Val	Glu	Asp	Glu	Ile	Ser	Leu	Ser	Ala	Tyr	Ile	Thr	Ile	Ala	Leu		
				565					570					575			
Leu	Glu	Met	Ser	Leu	Pro	Asp	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu		
			580					585					590				
Phe	Cys	Leu	Glu	Ser	Ala	Trp	Lys	Ser	Ala	Lys	Glu	Gly	Thr	His	Gly		
		595					600					605					
Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala		
	610					615					620						
Gly	Asn	Gln	Glu	Arg	Lys	Lys	Glu	Ile	Leu	Lys	Ser	Leu	Glu	Asp	Glu		
625					630					635					640		
Gly	Val	Lys	Glu	Asp	Asn	Ser	Leu	His	Trp	Ala	Arg	Pro	Gln	Lys	Pro		
				645					650					655			
Lys	Val	Ser	Glu	Gly	Phe	Leu	Phe	Lys	Ser	Gln	Ala	Pro	Ser	Ala	Glu		
			660					665					670				
Val	Glu	Met	Thr	Ser	Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Arg	Pro		
		675					680					685					
Ala	Pro	Thr	Pro	Glu	Asp	Leu	Thr	Ser	Ala	Thr	Asp	Ile	Val	Asn	Trp		
	690					695					700						
Val	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly	Tyr	Ser	Ser	Thr	Gln	Asp		
705					710					715					720		
Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	Tyr	Ala	Ala	Ala	Thr	Phe		
				725					730					735			
Thr	Arg	Thr	Glu	Lys	Ala	Ala	Gln	Val	Thr	Ile	Lys	Ser	Ser	Gly	Thr		
			740					745					750				



Phe	Ser	Thr	Asn	Phe	Glu	Val	Asn	His	Asn	Asn	Arg	Leu	Leu	Leu	Gln
		755					760					765			
Gln	Val	Ser	Leu	Pro	Thr	Val	Ser	Asp	Ser	Tyr	Thr	Ile	Thr	Val	Thr
	770					775					780				
Gly	Glu	Gly	Asn	Val	Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Val	Pro
785					790					795					800
Ser	Glu	Lys	Gly	Thr	Phe	Pro	Phe	Ala	Leu	Glu	Ala	Glu	Thr	Val	Pro
				805					810					815	
Gln	Ala	Cys	Asp	Gly	Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu
			820					825					830		
Asn	Val	Ser	Tyr	Ile	Gly	Ser	Arg	Pro	Val	Ser	Asn	Met	Ala	Ile	Val
		835					840					845			
Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys
	850					855					860				
Asn	Leu	Glu	Lys	Ser	Glu	His	Ile	Ser	Arg	Thr	Glu	Val	Ser	Asn	Asn
865					870					875					880
His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu
				885					890					895	
Ser	Phe	Phe	Val	Val	Gln	Asp	Ile	Glu	Val	Arg	Asp	Leu	Lys	Pro	Ala
			900					905					910		
Ile	Ile	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Thr	Asn	Glu	Phe	Ala	Ile	Ala
		915					920					925			
Glu	Tyr	His	Ala	Pro	Cys	Ser	Lys	Asp	Pro	Gly	Asn	Ala			
	930					935					940				

<210> 40  
 <211> 373  
 <212> PRT  
 <213> Mus musculus

<400> 40															
Met	Ser	Thr	Asp	Cys	Ala	Gly	Asn	Ser	Thr	Cys	Pro	Val	Asn	Ser	Thr
1				5					10					15	
Glu	Glu	Asp	Pro	Pro	Val	Gly	Met	Glu	Gly	His	Ala	Asn	Leu	Lys	Leu
			20				25						30		
Leu	Phe	Thr	Val	Leu	Ser	Ala	Val	Met	Val	Gly	Leu	Val	Met	Phe	Ser
			35				40					45			
Phe	Gly	Cys	Ser	Val	Glu	Ser	Gln	Lys	Leu	Trp	Leu	His	Leu	Arg	Arg
	50					55					60				
Pro	Trp	Gly	Ile	Ala	Val	Gly	Leu	Leu	Ser	Gln	Phe	Gly	Leu	Met	Pro
65					70					75				80	

Leu	Thr	Ala	Tyr	Leu	Leu	Ala	Ile	Gly	Phe	Gly	Leu	Lys	Pro	Phe	Gln	
				85					90					95		
Ala	Ile	Ala	Val	Leu	Met	Met	Gly	Ser	Cys	Pro	Gly	Gly	Thr	Ile	Ser	
			100					105					110			
Asn	Val	Leu	Thr	Phe	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Ile	Ser	
		115					120					125				
Met	Thr	Thr	Cys	Ser	Thr	Val	Ala	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys	
	130					135					140					
Leu	Tyr	Ile	Tyr	Thr	Arg	Ser	Trp	Thr	Leu	Thr	Gln	Asn	Leu	Val	Ile	
145					150					155					160	
Pro	Tyr	Gln	Ser	Ile	Gly	Ile	Thr	Leu	Val	Ser	Leu	Val	Val	Pro	Val	
				165					170					175		
Ala	Ser	Gly	Val	Tyr	Val	Asn	Tyr	Arg	Trp	Pro	Lys	Gln	Ala	Thr	Val	
			180					185					190			
Ile	Leu	Lys	Val	Gly	Ala	Ile	Leu	Gly	Gly	Met	Leu	Leu	Leu	Val	Val	
		195					200					205				
Ala	Val	Thr	Gly	Met	Val	Leu	Ala	Lys	Gly	Trp	Asn	Thr	Asp	Val	Thr	
	210					215					220					
Leu	Leu	Val	Ile	Ser	Cys	Ile	Phe	Pro	Leu	Val	Gly	His	Val	Thr	Gly	
225					230					235					240	
Phe	Leu	Leu	Ala	Phe	Leu	Thr	His	Gln	Ser	Trp	Gln	Arg	Cys	Arg	Thr	
				245					250					255		
Ile	Ser	Ile	Glu	Thr	Gly	Ala	Gln	Asn	Ile	Gln	Leu	Cys	Ile	Ala	Met	
			260					265					270			
Leu	Gln	Leu	Ser	Phe	Ser	Ala	Glu	Tyr	Leu	Val	Gln	Leu	Leu	Asn	Phe	
		275					280					285				
Ala	Leu	Ala	Tyr	Gly	Leu	Phe	Gln	Val	Leu	His	Gly	Leu	Leu	Ile	Val	
	290					295					300					
Ala	Ala	Tyr	Gln	Ala	Tyr	Lys	Arg	Arg	Gln	Lys	Ser	Lys	Cys	Arg	Arg	
305					310					315					320	
Gln	His	Pro	Asp	Cys	Pro	Asp	Val	Cys	Tyr	Glu	Lys	Gln	Pro	Arg	Glu	
				325					330					335		
Thr	Ser	Ala	Phe	Leu	Asp	Lys	Gly	Asp	Glu	Ala	Ala	Val	Thr	Leu	Gly	
			340					345					350			
Pro	Val	Gln	Pro	Glu	Gln	His	His	Arg	Ala	Ala	Glu	Leu	Thr	Ser	His	
		355					360					365				
Ile	Pro	Ser	Cys	Glu												
				370												

<210> 41  
 <211> 347  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 41

Met	Ser	Asn	Leu	Thr	Val	Gly	Cys	Leu	Ala	Asn	Ala	Thr	Val	Cys	Glu
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Gly	Ala	Ser	Cys	Val	Ala	Pro	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Ser
			20					25					30		
Val	Val	Leu	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Leu	Val	Met	Phe
		35					40					45			
Ser	Met	Gly	Cys	Asn	Val	Glu	Ile	Lys	Lys	Phe	Leu	Gly	His	Ile	Arg
	50					55					60				
Arg	Pro	Trp	Gly	Ile	Phe	Ile	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met
65				70						75					80
Pro	Leu	Thr	Gly	Phe	Val	Leu	Ala	Val	Ala	Phe	Gly	Ile	Met	Pro	Ile
				85					90					95	
Gln	Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Ala
			100					105					110		
Ser	Asn	Ile	Leu	Ala	Tyr	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val
		115					120					125			
Ser	Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu
	130					135					140				
Cys	Leu	Tyr	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val
145					150					155					160
Ile	Pro	Tyr	Asp	Asn	Ile	Gly	Thr	Ser	Leu	Val	Ala	Leu	Val	Val	Pro
			165						170					175	
Val	Ser	Ile	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys
			180					185					190		
Ile	Ile	Leu	Lys	Val	Gly	Ser	Ile	Ala	Gly	Ala	Val	Leu	Ile	Val	Leu
		195					200					205			
Ile	Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu
	210					215					220				
Pro	Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Met	Ala	Gly	Tyr	Ser
225					230					235					240
Leu	Gly	Phe	Phe	Leu	Ala	Arg	Ile	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys
			245						250					255	
Arg	Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser

260	265	270
Thr Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Thr Tyr Val Phe		
275	280	285
Thr Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile		
290	295	300
Phe Leu Gly Ile Tyr Val Ala Tyr Arg Lys Cys His Gly Lys Asn Asp		
305	310	315
Ala Glu Phe Pro Asp Ile Lys Asp Thr Lys Thr Glu Pro Glu Ser Ser		
	325	330
		335
Phe His Gln Met Asn Gly Gly Phe Gln Pro Glu		
340	345	

<210> 42  
 <211> 348  
 <212> PRT  
 <213> Rattus norvegicus

<400> 42

Met Asp Asn Ser Ser Val Cys Ser Pro Asn Ala Thr Phe Cys Glu Gly		
1	5	10
		15
Asp Ser Cys Leu Val Thr Glu Ser Asn Phe Asn Ala Ile Leu Ser Thr		
	20	25
		30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser		
	35	40
		45
Met Gly Cys Asn Val Glu Ile Asn Lys Phe Leu Gly His Ile Lys Arg		
50	55	60
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro		
65	70	75
		80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln		
	85	90
		95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser		
	100	105
		110
Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser		
115	120	125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys		
130	135	140
Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile		
145	150	155
		160
Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val		
	165	170
		175

Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile  
 180 185 190  
 Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile  
 195 200 205  
 Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro  
 210 215 220  
 Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu  
 225 230 235 240  
 Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg  
 245 250 255  
 Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr  
 260 265 270  
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr  
 275 280 285  
 Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Ile Ile  
 290 295 300  
 Leu Gly Met Tyr Val Thr Tyr Lys Lys Cys His Gly Lys Asn Asp Ala  
 305 310 315 320  
 Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe  
 325 330 335  
 Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
 340 345

<210> 43  
 <211> 348  
 <212> PRT  
 <213> Mus musculus

<400> 43  
 Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly  
 1 5 10 15  
 Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr  
 20 25 30  
 Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser  
 35 40 45  
 Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg  
 50 55 60  
 Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro  
 65 70 75 80  
 Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln  
 85 90 95

Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Gly	Ser		
			100					105					110				
Asn	Ile	Leu	Ala	Tyr	Trp	Ile	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val	Ser		
		115					120					125					
Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys		
	130					135					140						
Leu	Phe	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val	Ile		
145					150					155					160		
Pro	Tyr	Asp	Ser	Ile	Gly	Ile	Ser	Leu	Val	Ala	Leu	Val	Ile	Pro	Val		
			165						170					175			
Ser	Phe	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile		
		180						185					190				
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Thr	Gly	Val	Ile	Leu	Ile	Val	Leu	Ile		
		195					200					205					
Ala	Val	Ile	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro		
	210					215					220						
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu		
225					230					235					240		
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg		
			245					250						255			
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr		
		260					265						270				
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr		
	275						280					285					
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Val	Ile		
	290					295					300						
Leu	Gly	Ile	Tyr	Val	Thr	Tyr	Arg	Lys	Cys	Tyr	Gly	Lys	Asn	Asp	Ala		
305					310					315					320		
Glu	Phe	Leu	Glu	Lys	Thr	Asp	Asn	Glu	Met	Asp	Ser	Arg	Pro	Ser	Phe		
			325					330					335				
Asp	Glu	Thr	Asn	Lys	Gly	Phe	Gln	Pro	Asp	Glu	Lys						
		340					345										

<210> 44

<211> 348

<212> PRT

<213> Mus musculus

<400> 44

Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly

1		5		10		15											
Asp	Ser	Cys	Val	Val	Pro	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Asn	Thr		
			20					25					30				
Val	Met	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Met	Val	Met	Phe	Ser		
		35					40					45					
Met	Gly	Cys	Asn	Val	Glu	Val	His	Lys	Phe	Leu	Gly	His	Ile	Lys	Arg		
	50					55					60						
Pro	Trp	Gly	Ile	Phe	Val	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met	Pro		
65					70					75					80		
Leu	Thr	Gly	Phe	Ile	Leu	Ser	Val	Ala	Ser	Gly	Ile	Leu	Pro	Val	Gln		
				85					90					95			
Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Gly	Ser		
			100					105					110				
Asn	Ile	Leu	Ala	Tyr	Trp	Ile	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val	Ser		
		115					120					125					
Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys		
	130					135					140						
Leu	Phe	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val	Ile		
145					150					155					160		
Pro	Tyr	Asp	Ser	Ile	Gly	Ile	Ser	Leu	Val	Ala	Leu	Val	Ile	Pro	Val		
				165					170					175			
Ser	Phe	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile		
			180					185					190				
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Thr	Gly	Val	Ile	Leu	Ile	Val	Leu	Ile		
		195					200					205					
Ala	Val	Ile	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro		
						215					220						
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu		
225					230					235					240		
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg		
				245					250					255			
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr		
			260					265					270				
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr		
		275					280					285					
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Val	Ile		
	290					295					300						
Leu	Gly	Ile	Tyr	Val	Thr	Tyr	Arg	Lys	Cys	Tyr	Gly	Lys	Asn	Asp	Ala		

305		310		315		320
Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe						
		325		330		335
Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys						
		340		345		
<210> 45						
<211> 348						
<212> PRT						
<213> Homo sapiens						
<400> 45						
Met Asp Asn Ser Ser Ile Cys Asn Pro Asn Ala Thr Ile Cys Glu Gly						
1		5		10		15
Asp Ser Cys Ile Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser Val						
		20		25		30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe Ser						
		35		40		45
Met Gly Cys Asn Val Glu Leu His Lys Phe Leu Gly His Leu Arg Arg						
		50		55		60
Pro Trp Gly Ile Val Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro						
		65		70		75
Leu Thr Gly Phe Val Leu Ser Val Ala Phe Gly Ile Leu Pro Val Gln						
		85		90		95
Ala Val Val Val Leu Ile Gln Gly Cys Cys Pro Gly Gly Thr Ala Ser						
		100		105		110
Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val Ser						
		115		120		125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys						
		130		135		140
Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile						
		145		150		155
Pro Tyr Asp Ser Ile Gly Thr Ser Leu Val Ala Leu Val Ile Pro Val						
		165		170		175
Ser Ile Gly Met Tyr Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile						
		180		185		190
Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile						
		195		200		205
Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Thr Ile Glu Pro						
		210		215		220



Lys Leu Trp Ile Ile Gly Thr Ile Tyr Pro Ile Ala Gly Tyr Gly Leu  
 225 230 235 240  
 Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys Arg  
 245 250 255  
 Thr Val Ala Leu Glu Thr Gly Leu Gln Asn Thr Gln Leu Cys Ser Thr  
 260 265 270  
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr  
 275 280 285  
 Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile Leu  
 290 295 300  
 Leu Gly Ala Tyr Val Ala Tyr Lys Lys Cys His Gly Lys Asn Asn Thr  
 305 310 315 320  
 Glu Leu Gln Glu Lys Thr Asp Asn Glu Met Glu Pro Arg Ser Ser Phe  
 325 330 335  
 Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
 340 345

<210> 46  
 <211> 272  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu  
 1 5 10 15  
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala  
 20 25 30  
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile  
 35 40 45  
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro  
 50 55 60  
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr  
 65 70 75 80  
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe  
 85 90 95  
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr Ser Ile Gly Glu  
 100 105 110  
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys  
 115 120 125  
 Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu  
 130 135 140

Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr  
 145 150 155 160  
 Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly  
 165 170 175  
 Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu  
 180 185 190  
 Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys  
 195 200 205  
 Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile  
 210 215 220  
 Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys  
 225 230 235 240  
 Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn  
 245 250 255  
 Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln  
 260 265 270

<210> 47  
 <211> 272  
 <212> PRT  
 <213> Rattus norvegicus

<400> 47  
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu  
 1 5 10 15  
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala  
 20 25 30  
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile  
 35 40 45  
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro  
 50 55 60  
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr  
 65 70 75 80  
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe  
 85 90 95  
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Tyr Thr Ser Ile Gly Glu  
 100 105 110  
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys

115							120						125			
Ser	Val	Val	Ala	Arg	Phe	Asp	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Arg	Glu	
130						135					140					
Leu	Val	Ser	Arg	Gln	Val	Ser	Asp	Asp	Leu	Thr	Glu	Arg	Ala	Ala	Thr	
145					150					155					160	
Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	His	Leu	Thr	Phe	Gly	
				165					170					175		
Lys	Glu	Phe	Thr	Glu	Ala	Val	Glu	Ala	Lys	Gln	Val	Ala	Gln	Gln	Glu	
			180					185					190			
Ala	Glu	Arg	Ala	Arg	Phe	Val	Val	Glu	Lys	Ala	Glu	Gln	Gln	Lys	Lys	
		195					200					205				
Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Ala	Ala	Glu	Leu	Ile	
	210					215					220					
Ala	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu	Arg	Lys	
225					230					235					240	
Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ala	Tyr	Gln	Leu	Ser	Arg	Ser	Arg	Asn	
				245					250					255		
Ile	Thr	Tyr	Leu	Pro	Ala	Gly	Gln	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln	
			260					265					270			

<210> 48  
 <211> 1798  
 <212> PRT  
 <213> *Drosophila melanogaster*

<400> 48																
Met	Glu	Met	Arg	Glu	Val	Leu	Ser	Arg	Glu	Gly	Arg	Glu	Ala	Lys	Asn	
1				5					10					15		
Leu	Leu	Val	Tyr	Gln	Phe	Cys	Asp	Glu	Thr	Thr	Ser	Ser	Gly	Ala	Thr	
			20					25					30			
Ser	Gly	Phe	Gly	Ser	Thr	Gly	Gly	Asp	Val	Gly	Gly	Gly	Ser	Gly	Gly	
		35					40					45				
Asp	Gly	Pro	Ala	Val	Gly	Ser	Gly	Gly	Val	Leu	Leu	Asn	Gly	Asp	Cys	
	50					55					60					
Tyr	Arg	Lys	Pro	Pro	Met	Val	Pro	Pro	Lys	Ser	Pro	Asn	Gly	Thr	Pro	
65					70					75					80	
Lys	Asn	Cys	Gln	Ser	Pro	Thr	Ser	Pro	Arg	Leu	Lys	Ser	Ser	Ala	Ser	
				85					90					95		

Val	Gly	Cys	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Pro	Arg	Val	Arg	Ser	Ala				
			100					105					110						
Ser	Thr	Gly	Arg	Asp	Lys	Lys	Ser	Glu	Leu	Gln	Ala	Arg	Tyr	Trp	Ala				
		115					120					125							
Leu	Leu	Phe	Gly	Asn	Leu	Gln	Arg	Ala	Ile	Asn	Glu	Ile	Tyr	Gln	Thr				
	130					135					140								
Val	Glu	Cys	Tyr	Glu	Asn	Ile	Ser	Ser	Cys	Gln	Glu	Thr	Ile	Leu	Val				
145					150					155					160				
Leu	Glu	Asn	Tyr	Val	Arg	Asp	Phe	Lys	Ala	Leu	Cys	Glu	Trp	Phe	Lys				
				165					170					175					
Val	Ser	Trp	Asp	Tyr	Glu	Ser	Arg	Pro	Leu	Gln	Gln	Arg	Pro	Gln	Ser				
			180					185					190						
Leu	Ala	Trp	Glu	Val	Arg	Lys	Ser	Asn	Pro	Thr	Pro	Arg	Val	Arg	Thr				
		195					200					205							
Arg	Ser	Leu	Cys	Ser	Pro	Asn	Asn	Ser	Gly	Lys	Ser	Ser	Pro	Ala	Leu				
	210					215					220								
Phe	Pro	Gly	Thr	Gln	Ser	Gly	Glu	Thr	Ser	Pro	Phe	Cys	Asp	Asn	Gly				
225				230					235						240				
Gln	Ile	Ser	Pro	Arg	Lys	Leu	Leu	Arg	Ala	Tyr	Asp	Gln	Val	Pro	Lys				
				245					250					255					
Gly	Ala	Met	Arg	Leu	Asn	Val	Arg	Glu	Leu	Phe	Ala	Ala	Ser	Lys	Arg				
			260					265					270						
Ala	Thr	Gln	Gly	Ser	Ser	Gln	Ser	Asp	Asn	Met	Glu	Gly	Pro	Leu	Asp				
		275					280					285							
Leu	Ser	Gly	Asp	Lys	Ser	Asn	Phe	Val	Leu	Arg	Ser	Thr	Gln	Tyr	Ala				
	290					295					300								
Gln	Thr	Asp	Leu	Glu	Asp	Pro	His	Leu	Thr	Leu	Ala	Asp	Val	Arg	Glu				
305				310						315					320				
Lys	Met	Arg	Met	Glu	Ala	Glu	Glu	Arg	Glu	Ala	Gln	Asn	Arg	Ile	Glu				
				325					330					335					
Asn	Glu	Ala	Leu	Glu	Glu	Val	Thr	Ile	Pro	Ile	Asp	Asn	Glu	Asp	Ala				
			340					345					350						
Thr	Glu	Ser	Leu	Asn	Lys	Gln	Glu	Pro	Ser	Ser	Leu	Glu	Leu	Pro	Ile				
		355					360					365							
His	Asn	Val	Ala	Asp	Leu	Ser	Lys	Glu	Pro	Glu	Leu	Met	Glu	Ala	Ala				
	370					375					380								
Ser	Glu	Ala	Thr	Ala	Leu	Glu	Met	Thr	Val	Ala	Ser	Leu	Glu	Ser	Met				
385				390						395					400				

Glu	Asn	Ala	Leu	Leu	Asn	Gln	Gln	Ala	Asn	Lys	Glu	Pro	Thr	Pro	Pro	
				405					410					415		
Ser	Thr	Val	Ile	Lys	Pro	Leu	Ala	Glu	Ile	Leu	Lys	Lys	Pro	Gln	Pro	
			420					425					430			
Leu	Asn	Pro	Leu	Ser	Gly	Asn	Asn	Val	Gln	Asn	Ser	Pro	Leu	Lys	Tyr	
		435					440					445				
Ser	Ser	Val	Leu	Asn	Arg	Pro	Ser	Lys	Lys	Met	Ile	Pro	Pro	Pro	Gly	
		450				455					460					
Gly	Val	Ala	Ala	Gln	Lys	Thr	Ile	Ser	Thr	Lys	Pro	Gly	Leu	Val	Lys	
465					470					475					480	
Pro	Asn	Leu	Thr	Thr	Thr	Val	Asn	Gly	Leu	Arg	Ser	Thr	Lys	Thr	Ala	
				485					490					495		
Thr	Ala	Pro	Pro	Ala	Ile	Lys	Thr	Thr	Gly	Arg	Ser	Gly	Leu	Gln	Arg	
			500					505					510			
His	Pro	Arg	Pro	Ser	Ser	Lys	Thr	Glu	Cys	Tyr	Gly	Pro	Pro	Asn	Asn	
		515					520					525				
Val	Ala	Ser	Arg	Leu	Ser	Ala	Arg	Ser	Arg	Thr	Ile	Asn	Thr	Leu	Lys	
		530				535					540					
Ala	Glu	Asn	Gln	His	Ser	Glu	Pro	Lys	Gln	Ile	Gln	Pro	Pro	Thr	Asp	
545					550					555					560	
Ala	Asp	Asp	Gly	Trp	Leu	Thr	Val	Lys	Asn	Arg	Arg	Arg	Thr	Ser	Met	
				565					570					575		
His	Trp	Ala	Asn	Arg	Phe	Asn	Gln	Pro	Thr	Gly	Tyr	Ala	Ser	Leu	Pro	
			580					585					590			
Thr	Leu	Ala	Leu	Leu	Asn	Glu	Gln	Gln	Lys	Glu	Gln	Glu	His	Lys	Glu	
		595					600					605				
Lys	Gln	Lys	Gly	Glu	Asp	Asp	Gly	Lys	Val	Ile	Val	Lys	Thr	Ile	Ser	
	610					615					620					
Ala	Lys	Thr	Lys	Ala	Pro	Ile	Glu	Val	Ala	Lys	Ala	Lys	Ala	Lys	Thr	
625					630					635					640	
Ser	Ile	Val	Ile	Thr	Arg	Pro	Glu	Ile	Lys	Asn	Ala	Lys	Ala	Lys	Val	
				645					650					655		
Asn	Ser	Phe	Pro	Val	Gln	Lys	Ser	Asn	Thr	Asn	Gln	Val	Lys	Lys	Pro	
			660					665					670			
Glu	Lys	Gln	Glu	Lys	Ser	Asp	Thr	Thr	Ala	Pro	Ala	Ala	Ile	Ala	Ser	
		675					680					685				
Ser	Arg	Leu	Lys	Met	Thr	Ser	Leu	His	Lys	Glu	Tyr	Met	Arg	Ser	Glu	
		690				695					700					

Lys	Asn	Ala	Leu	Arg	Lys	Leu	Gln	Gln	Lys	Glu	Gln	Gly	Asn	Gln	Gln	
705					710					715					720	
His	Asn	Ser	Ser	Ser	Ser	Ser	Ala	Glu	Thr	Val	Val	Glu	Ser	Cys	Asn	
				725					730					735		
Glu	Asp	His	Ser	Lys	Ile	Asp	Ile	Lys	Ile	Gln	Thr	Asn	Cys	Glu	Phe	
			740					745					750			
Ser	Lys	Thr	Ile	Gly	Glu	Leu	Tyr	Glu	Ser	Ile	Ala	His	Cys	Lys	Leu	
		755					760					765				
Pro	Ser	Gly	Ser	Leu	Lys	Thr	Asn	Ala	Ser	Thr	Leu	Ser	Ala	Cys	Asp	
	770					775					780					
Glu	Asn	Glu	Glu	Gln	Asn	Thr	Asp	Asp	Asn	Glu	Glu	Glu	Arg	Asn	Glu	
785					790					795					800	
Arg	Ile	Leu	Gly	Glu	Val	Gln	Glu	Ser	Leu	Glu	Arg	Gln	Ile	Arg	Glu	
				805					810					815		
Leu	Glu	Gln	Thr	Glu	Ile	Asp	Val	Asp	Thr	Glu	Thr	Asp	Glu	Thr	Asp	
			820					825					830			
Cys	Glu	Val	Gln	Leu	Glu	Glu	Gln	Asp	Asp	Gly	Val	Asp	Gly	Leu	Glu	
		835					840					845				
Met	Gly	Ser	Gly	Asp	Asp	Ser	Ala	Val	Phe	Val	Thr	Met	Ser	Asp	Asp	
	850					855					860					
Glu	Asn	Ala	Ser	Leu	Glu	Leu	Arg	Tyr	Gln	Ala	Leu	Leu	Ser	Asp	Met	
865					870					875					880	
Ser	Trp	Asn	Glu	Arg	Ala	Glu	Ala	Leu	Ala	Thr	Leu	Gln	Ala	Tyr	Val	
				885					890					895		
Ala	Arg	His	Pro	Gly	Arg	Ala	Gln	Glu	Leu	His	Gln	Lys	Leu	Ser	Ser	
			900					905					910			
Pro	Ser	Arg	Arg	Arg	Ser	Leu	Gln	Glu	Thr	Leu	Lys	Lys	Tyr	Gln	Ala	
		915					920					925				
Lys	Gln	Ala	Arg	Ala	Gln	Gln	Lys	Arg	Asn	Leu	Leu	Gln	Gln	Glu	Lys	
	930					935					940					
Ala	Ala	Lys	Leu	Gln	Gln	Leu	Phe	Ser	Arg	Val	Glu	Asp	Val	Lys	Ala	
945					950					955					960	
Ala	Lys	Asn	Gln	Ile	Ile	Glu	Asp	Lys	Arg	Gln	Lys	Met	Gln	Gly	Arg	
				965					970					975		
Leu	Gln	Arg	Ala	Ala	Glu	Asn	Arg	Glu	Gln	Tyr	Leu	Lys	Gln	Ile	Ile	
			980					985					990			
Glu	Lys	Ala	His	Asp	Glu	Glu	Lys	Lys	Leu	Lys	Glu	Ile	Asn	Phe	Ile	
		995					1000					1005				

Lys Asn Ile Glu Ala Gln Asn Lys Arg Leu Asp Leu Leu Glu Ser Ser  
 1010 1015 1020  
 Lys Glu Thr Glu Gly Arg Leu Gln Asp Leu Glu Gln Glu Arg Gln Lys  
 1025 1030 1035 1040  
 Arg Val Glu Glu Lys Leu Ala Lys Glu Ala Ala Val Glu Arg Arg Arg  
 1045 1050 1055  
 Gln Ala Leu Glu Lys Glu Arg Leu Leu Lys Leu Glu Lys Met Asn Glu  
 1060 1065 1070  
 Thr Arg Leu Glu Lys Glu Gln Arg Ile Gly Lys Met Gln Glu Gln Lys  
 1075 1080 1085  
 Glu Lys Gln Arg Gln Ala Leu Ala Arg Glu Lys Ala Arg Asp Arg Glu  
 1090 1095 1100  
 Glu Arg Leu Leu Ala Leu Gln Val Gln Gln Gln Gln Thr Thr Glu Glu  
 1105 1110 1115 1120  
 Leu Gln Arg Lys Ile Leu Gln Lys Gln Met Glu Ser Ala Arg Arg His  
 1125 1130 1135  
 Glu Glu Asn Ile Glu His Ile Arg Gln Arg Ala Leu Glu Leu Thr Ile  
 1140 1145 1150  
 Pro Thr Arg Gln Ala Asp Glu Gly Arg Gly Asp Gln Asp Val Ser Glu  
 1155 1160 1165  
 Asp Ile Leu Asn Gly Asn Ala Thr Ser Thr Thr Asn Glu Asp Cys Asp  
 1170 1175 1180  
 Leu Ser Ser Ser Leu Ser Glu Val Gly Gly Asn Asn Ala His Thr Arg  
 1185 1190 1195 1200  
 Ser Tyr Lys Lys Lys Met Lys Lys Leu Lys Gln Arg Met Asn Gln Cys  
 1205 1210 1215  
 Ala Ala Glu Tyr Leu Glu Ser Leu Glu Ala Leu Pro Ala His Ala Arg  
 1220 1225 1230  
 Arg Asp Ser Thr Val Pro Lys Leu Leu Asn Leu Val Val Lys Gly Gly  
 1235 1240 1245  
 Gly Ala Gln Gly Leu Asp Arg Asn Leu Gly Asn Leu Leu Arg Val Ile  
 1250 1255 1260  
 Pro Lys Ala Gln Thr Leu Asp Phe Leu Ala Phe Leu Cys Met Asp Gly  
 1265 1270 1275 1280  
 Leu Gly Ile Leu Ala Asn His Val Ile Ser Lys Gly Met Asp Glu Asn  
 1285 1290 1295  
 Ser Glu Ile Ser Arg Lys Ser Val Tyr Leu Ala Ala Gln Leu Tyr Arg  
 1300 1305 1310

Asn Ala Cys Ser Val Cys Pro Gln Ile Ala Arg His Ala Leu Leu Gly  
 1315 1320 1325  
 Asn Ser Ile Thr Val Leu Phe Asp Ala Ile Asn Lys Ser Phe Gln Val  
 1330 1335 1340  
 Ile Leu Lys Ser Asn Arg Cys Thr Lys Glu Thr Phe Ser Asn Phe Trp  
 1345 1350 1355 1360  
 Pro Pro Lys Met Leu His Asn Lys Ser Val Ala Arg Gln Ser Ser Arg  
 1365 1370 1375  
 Leu Glu Ala Leu Ser Leu Pro Glu Glu Lys Ser Pro Gln His Pro Val  
 1380 1385 1390  
 Glu Leu Ser Thr Glu Leu Met Leu Ala Cys Thr Glu Ala Leu Ser Ser  
 1395 1400 1405  
 Ser Tyr Val Lys Lys Asn Thr His Pro Lys Val Pro Glu Arg Leu Pro  
 1410 1415 1420  
 Asp Met Ile Asn Asp Cys Arg Phe His Trp Gln Asp Val Asn Lys Glu  
 1425 1430 1435 1440  
 Asp Met Leu Ala Asp Glu Phe Arg Lys Tyr Lys Cys Tyr Glu Lys Asn  
 1445 1450 1455  
 Pro Val Ile Ala Leu Pro His Pro Ser Leu Ser Ala Ser Leu Cys Arg  
 1460 1465 1470  
 Ser Leu Ser Ala Thr Pro Leu Lys Ile Asn Leu His Gln Phe Leu Gly  
 1475 1480 1485  
 Ser Gly Ile Leu Ile Leu Arg Leu Asn His His Arg His Pro Ala Thr  
 1490 1495 1500  
 Gly Ala Ser Phe Ser Asp Ser Cys Cys Thr Cys Cys Pro Lys Leu Thr  
 1505 1510 1515 1520  
 Thr Glu Ala Ala Val Ala Ala Val Ala Ala His Gln His Gln His Gln  
 1525 1530 1535  
 Asn Gln Gln Gln Gln Pro Asp Tyr Ala Val Ile Thr Gly Leu Ile Glu  
 1540 1545 1550  
 Ile Leu Ser Arg Arg Ile Gln Lys Val Arg Glu Ser Ile Glu Ser Asn  
 1555 1560 1565  
 Lys Ser Val Met Leu Ser Leu Leu Thr Thr Leu Gly Phe Leu Ser Arg  
 1570 1575 1580  
 Phe Ile Asp Val Cys Gln Pro Gly Pro Ala Asp Pro Thr Arg Leu Leu  
 1585 1590 1595 1600  
 Ser Ala Ala Lys Ser Thr Glu Leu Phe Gly Thr Val Ser Met Leu Tyr  
 1605 1610 1615



Gly Cys Val Met Pro Met Gly Glu Cys Ile Pro Pro Arg Thr Thr Ala  
 1620 1625 1630  
 Leu Ala Ala Ser Thr Phe His Leu Tyr Val Ser Leu Ala Ser Leu Asp  
 1635 1640 1645  
 Val Asn Thr Phe Gln Glu Thr Leu Thr Val Glu Gly Pro Leu Ser Leu  
 1650 1655 1660  
 Lys Leu Leu Asp Val Met Thr Val Ile Leu Asn Cys Ser Leu Val Asn  
 1665 1670 1675 1680  
 Asp Gln Trp Thr Thr Asn Ser Glu Ser Cys Pro Met Leu Ile Asp Leu  
 1685 1690 1695  
 Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp  
 1700 1705 1710  
 Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys  
 1715 1720 1725  
 Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val  
 1730 1735 1740  
 Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp  
 1745 1750 1755 1760  
 Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn  
 1765 1770 1775  
 Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala  
 1780 1785 1790  
 Gly Asn Lys Lys Asn Ala  
 1795

<210> 49  
 <211> 274  
 <212> PRT  
 <213> Toxocara canis

<400> 49  
 Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val  
 1 5 10 15  
 Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val  
 20 25 30  
 Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys  
 35 40 45  
 Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln  
 50 55 60  
 Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr  
 65 70 75 80

Ile	Thr	Gly	Ser	Lys	Asp	Leu	Gln	Asn	Val	Ser	Ile	Thr	Leu	Arg	Ile	
				85					90					95		
Leu	His	Arg	Pro	Glu	Pro	Ser	Lys	Leu	Pro	Asn	Ile	Tyr	Leu	Asn	Ile	
			100					105					110			
Gly	Gln	Asp	Tyr	Ala	Glu	Arg	Val	Leu	Pro	Ser	Ile	Thr	Asn	Glu	Val	
		115					120					125				
Leu	Lys	Ala	Val	Val	Ala	Gln	Phe	Asp	Ala	His	Glu	Met	Ile	Thr	Gln	
	130					135					140					
Arg	Glu	Ser	Val	Ser	His	Arg	Val	Ser	Val	Glu	Leu	Ser	Glu	Arg	Ala	
145					150					155					160	
Arg	Gln	Phe	Gly	Ile	Leu	Leu	Asp	Asp	Ile	Ala	Ile	Thr	His	Leu	Ser	
				165					170					175		
Phe	Gly	Arg	Glu	Phe	Thr	Glu	Ala	Val	Glu	Met	Lys	Gln	Val	Ala	Gln	
			180					185					190			
Gln	Glu	Ala	Glu	Lys	Ala	Arg	Tyr	Leu	Val	Glu	Thr	Ala	Glu	Gln	Met	
		195					200					205				
Lys	Ile	Ala	Ala	Ile	Thr	Thr	Ala	Glu	Gly	Asp	Ala	Gln	Ala	Ala	Lys	
	210					215					220					
Leu	Leu	Ala	Gln	Ala	Phe	Lys	Asp	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu	
225					230					235					240	
Arg	Lys	Ile	Glu	Ala	Ala	Glu	Glu	Ile	Ala	Glu	Arg	Met	Ser	Lys	Thr	
				245					250					255		
Arg	Asn	Val	Ile	Tyr	Leu	Pro	Gly	Asn	Gln	Asn	Thr	Leu	Phe	Asn	Leu	
		260						265					270			

Pro Ala

<210> 50  
 <211> 402  
 <212> PRT  
 <213> Caenorhabditis elegans

<400> 50

Met	Glu	Lys	Tyr	Lys	Asn	Glu	Leu	Glu	Ile	Phe	Lys	Arg	Met	Tyr	Phe	
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Lys	Asn	Tyr	Pro	Thr	Ser	Ser	Lys	Asp	Glu	Glu	Ala	Ala	Ala	Val	Ile	
			20					25					30			
Gln	Lys	Gly	Gly	Glu	Phe	Ile	Gln	Glu	Ile	Leu	Pro	Thr	Ile	Ile	Ser	
		35					40					45				
Thr	Ser	Arg	Ala	Tyr	Asp	Thr	Asn	Gln	Lys	Ala	Leu	Leu	Leu	Ala	Glu	

50					55					60					
Gly	Gly	Lys	Met	Tyr	Asn	Val	Leu	Glu	Asp	Tyr	Asn	Glu	Thr	Ala	Glu
65					70					75					80
Lys	Met	Leu	Ser	Lys	Ser	Val	Arg	Met	Asn	Pro	Lys	Asn	Ala	Asp	Ala
				85					90					95	
Trp	His	Glu	Leu	Gly	Leu	Cys	Val	Met	Lys	Arg	Arg	Asp	Leu	Glu	Phe
			100					105					110		
Ala	Gln	Ser	Cys	Phe	Lys	Ile	Ala	Leu	Gly	Ile	Ser	Lys	Thr	Ala	Pro
		115					120					125			
Ile	Leu	Thr	Ser	Leu	Ala	Val	Ala	Met	Arg	Leu	Val	Ala	Leu	Glu	His
	130					135					140				
Pro	Glu	Pro	Ala	Gln	Ala	Glu	Ile	Arg	Thr	Lys	Ala	Met	Glu	Leu	Ile
145						150					155				160
Ile	Glu	Ala	Arg	Arg	Leu	Asp	Ser	Ala	Tyr	Gly	Pro	Ala	Asn	Ile	Ala
			165						170					175	
Phe	Ala	Thr	Gly	Leu	Phe	Tyr	Cys	Phe	Phe	Ser	Thr	Ala	Lys	Val	Glu
			180					185					190		
Leu	Lys	Phe	Leu	Asp	Lys	Val	Ile	Glu	Asn	Tyr	Lys	Lys	Ala	Leu	Glu
		195					200					205			
Cys	Glu	Leu	Ser	Arg	Thr	Asp	Pro	Gln	Val	Tyr	Ile	Asn	Met	Ala	Thr
	210					215					220				
Cys	Leu	Lys	Phe	Met	Glu	Lys	Tyr	Asp	Glu	Ala	Leu	Ala	Val	Leu	Gln
225						230					235				240
Lys	Ala	Val	Glu	Tyr	Asp	Pro	Arg	Asn	Glu	Leu	Glu	Thr	Arg	Glu	Lys
			245						250					255	
Leu	Ala	Ser	Phe	Val	Ser	Tyr	Leu	Ser	Lys	Phe	Thr	Asp	Ala	Ile	Gln
			260					265					270		
Lys	Lys	Gly	Lys	Met	Lys	Ala	Lys	Arg	Met	Gln	Glu	Met	Ile	Asn	Glu
		275					280					285			
Leu	Lys	Lys	Ser	Ser	Asp	Gly	Phe	Arg	Ala	Lys	Ile	Ile	Gly	Asn	Ile
	290					295					300				
Gly	His	Asp	Glu	Thr	Ile	Pro	Val	Ala	Leu	Val	Gly	Val	Asp	Ala	Ala
305						310					315				320
Gly	Glu	Val	Tyr	Gly	Ile	Thr	Ile	Tyr	Asn	Cys	Leu	Ser	Asn	Phe	Gly
			325						330					335	
Phe	Val	Ile	Gly	Asp	Thr	Val	Thr	Ile	Ala	Lys	Pro	Asp	Phe	Arg	Glu
			340					345					350		
Ile	Lys	Asn	Leu	Thr	Ile	Pro	Ser	Asp	Pro	Glu	Ile	His	Val	Asp	Ser

355		360		365
Val Lys Trp Ile Arg Val Ala Thr Pro Thr Gln Met Lys Lys Asn Gly				
370		375		380
Val Pro Leu Pro Glu Ser Val Leu Ala Arg Ala Val Ala Ser Thr Gln				
385		390		400
Thr Lys				
<210> 51				
<211> 711				
<212> PRT				
<213> Homo sapiens				
<400> 51				
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Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr				
	20		25	30
Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu				
	35		40	45
Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met				
	50		55	60
Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu				
	65		70	75 80
Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly				
		85		90 95
Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met				
	100		105	110
Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly				
	115		120	125
Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr				
	130		135	140
Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro				
	145		150	155 160
Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val				
		165		170 175
Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val				
	180		185	190
Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser				
	195		200	205

Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro			
210						215					220							
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys			
225					230					235					240			
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro			
				245					250					255				
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala			
			260					265					270					
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly			
		275					280					285						
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys			
	290					295					300							
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu			
305					310					315					320			
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp			
				325					330					335				
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala			
			340					345					350					
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln			
		355					360					365						
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys			
	370					375					380							
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His			
385					390					395					400			
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu			
				405					410					415				
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr			
			420					425					430					
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys			
		435					440					445						
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln			
	450					455					460							
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser			
465					470					475					480			
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val			
				485					490					495				
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val			
			500					505					510					

Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His  
 515 520 525  
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn  
 530 535 540  
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met  
 545 550 555 560  
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg  
 565 570 575  
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu  
 580 585 590  
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly  
 595 600 605  
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu  
 610 615 620  
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val  
 625 630 635 640  
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala  
 645 650 655  
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys  
 660 665 670  
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
 675 680 685  
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
 690 695 700  
 His Lys Val Met Arg Leu Gly  
 705 710

<210> 52  
 <211> 711  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val  
 1 5 10 15  
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
 20 25 30  
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
 35 40 45  
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
 50 55 60

Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Val	Ser	Ser	His	Gly	Cys	Gln	Leu	65	70	75	80
Leu	Pro	Trp	Thr	Gln	His	Ser	Pro	His	Thr	Arg	Leu	Arg	Arg	Ser	Gly	85	90	95	
Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met	100	105	110	
Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly	115	120	125	
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr	130	135	140	
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	145	150	155	160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	165	170	175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	180	185	190	
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	195	200	205	
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	210	215	220	
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	225	230	235	240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250	255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	260	265	270	
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	275	280	285	
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	290	295	300	
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	305	310	315	320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	325	330	335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	340	345	350	
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	355	360	365	

Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys	
370						375					380					
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	
385					390					395					400	
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	
				405					410					415		
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	
			420					425					430			
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	
		435					440					445				
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln	
	450					455					460					
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser	
465					470					475					480	
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val	
				485					490					495		
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val	
			500					505					510			
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His	
		515					520					525				
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn	
	530					535					540					
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met	
545					550					555					560	
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg	
				565					570					575		
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu	
			580					585					590			
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly	
		595					600					605				
Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val	Leu	Asn	Val	Ala	Phe	Leu	
	610					615					620					
Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile	Lys	His	Arg	Gly	Arg	Val	
625					630					635					640	
Arg	Glu	Ser	Glu	Met	Cys	Thr	Glu	Gly	Leu	Leu	Ala	Pro	Val	Gly	Ala	
				645					650					655		
Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys	Phe	Thr	His	Asn	Cys	
			660					665					670			



Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
675 680 685

Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
690 695 700

His Lys Val Met Arg Leu Gly  
705 710

<210> 53

<211> 711

<212> PRT

<213> Homo sapiens

<400> 53

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val  
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu  
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly  
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met  
100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly  
115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr  
130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro  
145 150 155 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val  
165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val  
180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser  
195 200 205

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro

210		215		220
Phe Glu Pro Gly Lys	Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys			
225	230	235		240
Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro				
	245	250		255
Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala				
	260	265		270
Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly				
	275	280		285
Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys				
	290	295		300
Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu				
305	310	315		320
Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp				
	325	330		335
Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala				
	340	345		350
Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln				
	355	360		365
Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys				
	370	375		380
Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His				
385	390	395		400
Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu				
	405	410		415
Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr				
	420	425		430
Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys				
	435	440		445
Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln				
	450	455		460
Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser				
465	470	475		480
Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val				
	485	490		495
Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val				
	500	505		510
Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His				

515	520	525
Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn		
530	535	540
Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met		
545	550	555
Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg		
	565	570
Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu		
	580	585
Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly		
	595	600
Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu		
	610	615
Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val		
625	630	635
Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala		
	645	650
Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys		
	660	665
Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser		
	675	680
Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile		
	690	695
His Lys Val Met Arg Leu Gly		
705	710	

<210> 54  
 <211> 529  
 <212> PRT  
 <213> Homo sapiens

<400> 54
Met Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln
1 5 10 15
Leu Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg His Ser
20 25 30
Gly Arg Cys Asp Leu Phe Gln Glu Lys Asp Tyr Ile Arg Thr Cys Ile
35 40 45
Met Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly
50 55 60

Gly	Leu	Ser	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Gln	65	70	75	80
Tyr	Met	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	85	90	95	
Pro	Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	His	Thr	Thr	Asp	Pro	Ala	100	105	110	
Val	Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Val	Ala	Ala	Cys	115	120	125	
Val	Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	130	135	140	
Ser	Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	145	150	155	160
Pro	Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	165	170	175	
Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	180	185	190	
Pro	Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	195	200	205	
Ala	Gln	Pro	Arg	Gln	Glu	Ala	Thr	Ser	Val	Ser	Cys	Phe	Arg	Gly	Lys	210	215	220	
Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	225	230	235	240
Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	245	250	255	
Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	260	265	270	
Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	275	280	285	
Val	Gly	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	290	295	300	
Gln	Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	305	310	315	320
Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Gly	Ser	Ala	Glu	Thr	Pro	325	330	335	
His	Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	340	345	350	
Glu	Asn	Phe	Cys	Gln	Thr	Gln	Met	Gly	Ile	Ala	Met	Gly	Pro	Gly	Ala	355	360	365	

Thr	Arg	Trp	Thr	Gln	Gly	Pro	His	Ser	Thr	Thr	Val	Pro	Cys	Asp	Ala	
370						375					380					
Ala	Leu	Met	Thr	Ser	Arg	His	Gln	Ser	Trp	Thr	Pro	Gln	Thr	Arg	Cys	
385					390					395					400	
Ser	Leu	Arg	Ser	Val	Ala	Arg	Gly	Trp	Ile	Gly	Trp	Ile	Ser	Val	Val	
				405					410					415		
Pro	Ser	Cys	Ala	Trp	Leu	Gly	Ala	Ile	Arg	Ala	Thr	His	Pro	Gly	Gln	
			420					425					430			
Ser	Ala	Cys	Gly	Ile	Gly	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	
		435					440					445				
Val	Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	
	450					455					460					
His	Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	
465					470					475					480	
Asn	Pro	Gln	His	Gly	Glu	Pro	Gly	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	
				485					490					495		
Met	Leu	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	
			500					505					510			
Arg	Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	
		515					520					525				

Glu

<210> 55  
 <211> 716  
 <212> PRT  
 <213> Mus musculus

<400> 55																
Met	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Val	Gln	Cys	Ser	Arg	Ala	
1				5					10					15		
Leu	Gly	Gln	Arg	Ser	Pro	Leu	Asn	Asp	Phe	Gln	Leu	Phe	Arg	Gly	Thr	
			20					25					30			
Glu	Leu	Arg	Asn	Leu	Leu	His	Thr	Ala	Val	Pro	Gly	Pro	Trp	Gln	Glu	
		35					40					45				
Asp	Val	Ala	Asp	Ala	Glu	Glu	Cys	Ala	Arg	Arg	Cys	Gly	Pro	Leu	Leu	
	50					55					60					
Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Met	Ser	Ser	His	Gly	Cys	Gln	Leu	
65					70					75					80	
Leu	Pro	Trp	Thr	Gln	His	Ser	Leu	His	Thr	Gln	Leu	Tyr	His	Ser	Ser	
				85					90					95		

Leu	Cys	His	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met		
			100					105					110				
Asp	Asn	Gly	Val	Ser	Tyr	Arg	Gly	Thr	Val	Ala	Arg	Thr	Ala	Gly	Gly		
		115					120					125					
Leu	Pro	Cys	Gln	Ala	Trp	Ser	Arg	Arg	Phe	Pro	Asn	Asp	His	Lys	Tyr		
	130					135					140						
Thr	Pro	Thr	Pro	Lys	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro		
145					150					155					160		
Asp	Gly	Asp	Pro	Arg	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asn	Arg	Ser	Val		
				165					170					175			
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Thr	Cys	Arg	Glu	Ala	Val	Cys	Val		
			180					185					190				
Leu	Cys	Asn	Gly	Glu	Asp	Tyr	Arg	Gly	Glu	Val	Asp	Val	Thr	Glu	Ser		
		195					200					205					
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Ser	His	Pro		
	210					215					220						
Phe	Gln	Pro	Glu	Lys	Phe	Leu	Asp	Lys	Asp	Leu	Lys	Asp	Asn	Tyr	Cys		
225					230					235					240		
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro		
				245					250					255			
Asn	Val	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Ser	Cys	Gly	Pro	Asn	Leu		
			260					265					270				
Pro	Pro	Thr	Val	Lys	Gly	Ser	Lys	Ser	Gln	Arg	Arg	Asn	Lys	Gly	Lys		
		275					280					285					
Ala	Leu	Asn	Cys	Phe	Arg	Gly	Lys	Gly	Glu	Asp	Tyr	Arg	Gly	Thr	Thr		
	290					295					300						
Asn	Thr	Thr	Ser	Ala	Gly	Val	Pro	Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ser		
305					310					315					320		
Pro	His	Gln	His	Arg	Phe	Val	Pro	Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu		
				325					330					335			
Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys		
			340					345					350				
Phe	Thr	Ser	Arg	Pro	Gly	Leu	Arg	Met	Ala	Phe	Cys	His	Gln	Ile	Pro		
		355					360					365					
Arg	Cys	Thr	Glu	Glu	Leu	Val	Pro	Glu	Gly	Cys	Tyr	His	Gly	Ser	Gly		
	370					375					380						
Glu	Gln	Tyr	Arg	Gly	Ser	Val	Ser	Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys		
385					390					395					400		

Gln	His	Trp	Ser	Ser	Glu	Thr	Pro	His	Lys	Pro	Gln	Phe	Thr	Pro	Thr		
				405					410					415			
Ser	Ala	Pro	Gln	Ala	Gly	Leu	Glu	Ala	Asn	Phe	Cys	Arg	Asn	Pro	Asp		
			420					425					430				
Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	Pro	Asp	Ile	Leu		
		435					440					445					
Phe	Asp	Tyr	Cys	Ala	Leu	Gln	Arg	Cys	Asp	Asp	Asp	Gln	Pro	Pro	Ser		
	450					455					460						
Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Val	Phe	Glu	Lys	Cys	Gly	Lys	Arg		
465					470					475					480		
Val	Asp	Lys	Ser	Asn	Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn		
				485					490					495			
Ser	Pro	Trp	Thr	Val	Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys		
			500					505					510				
Gly	Gly	Ser	Leu	Val	Lys	Glu	Gln	Trp	Val	Leu	Thr	Ala	Arg	Gln	Cys		
		515					520					525					
Ile	Trp	Ser	Cys	His	Glu	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly		
	530					535					540						
Thr	Ile	Asn	Gln	Asn	Pro	Gln	Pro	Gly	Glu	Ala	Asn	Leu	Gln	Arg	Val		
545				550						555					560		
Pro	Val	Ala	Lys	Ala	Val	Cys	Gly	Pro	Ala	Gly	Ser	Gln	Leu	Val	Leu		
				565				570						575			
Leu	Lys	Leu	Glu	Arg	Pro	Val	Ile	Leu	Asn	His	His	Val	Ala	Leu	Ile		
			580					585					590				
Cys	Leu	Pro	Pro	Glu	Gln	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu		
		595					600					605					
Ile	Ala	Gly	Trp	Gly	Glu	Ser	Ile	Gly	Thr	Ser	Asn	Asn	Thr	Val	Leu		
	610					615					620						
His	Val	Ala	Ser	Met	Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Thr	Lys		
625					630					635					640		
Tyr	Arg	Gly	His	Ile	Gln	Glu	Ser	Glu	Ile	Cys	Thr	Gln	Gly	Leu	Val		
				645					650					655			
Val	Pro	Val	Gly	Ala	Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys		
			660					665					670				
Tyr	Thr	His	Asp	Cys	Trp	Val	Leu	Gln	Gly	Leu	Ile	Ile	Pro	Asn	Arg		
		675					680					685					
Val	Cys	Ala	Arg	Pro	Arg	Trp	Pro	Ala	Ile	Phe	Thr	Arg	Val	Ser	Val		
	690					695					700						

Phe Val Asp Trp Ile Asn Lys Val Met Gln Leu Glu  
 705 710 715

<210> 56  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser  
 1 5 10 15  
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu  
 20 25 30  
 Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Val Thr Cys Asp  
 35 40 45  
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln  
 50 55 60  
 Phe Ser Cys Pro Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly  
 65 70 75 80  
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln  
 85 90 95  
 His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys  
 100 105 110  
 Asp Gly Lys Leu Val Val Glu Cys Val Met Asn His Val Ala Cys Thr  
 115 120 125  
 Arg Ile Tyr Glu Lys Val Glu  
 130 135

<210> 57  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 57  
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser  
 1 5 10 15  
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu  
 20 25 30  
 Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp  
 35 40 45  
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln  
 50 55 60



Phe	Ser	Cys	Thr	Leu	Gly	Glu	Lys	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70					75					80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Glu	Cys	Val	Met	Asn	Asn	Val	Thr	Cys	Thr
		115					120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									

<210> 58  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 58															
Met	Ala	Thr	Val	Gln	Gln	Leu	Glu	Gly	Arg	Trp	Arg	Leu	Val	Asp	Ser
1				5					10					15	
Arg	Gly	Phe	Asp	Glu	Tyr	Val	Lys	Glu	Leu	Gly	Val	Gly	Ile	Ala	Leu
			20					25					30		
Arg	Lys	Met	Asp	Thr	Ile	Ala	Lys	Pro	Asp	Cys	Ile	Ile	Thr	Cys	Asp
		35					40					45			
Gly	Lys	Asn	Leu	Thr	Ile	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln
	50					55					60				
Phe	Ser	Cys	Thr	Leu	Gly	Glu	Asn	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70					75					80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Asn	Thr	Ile	Arg	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Asp	Cys	Val	Met	Asn	Ser	Val	Thr	Cys	Thr
		115					120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									

<210> 59  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 59															
Met	Ala	Thr	Val	Gln	Gln	Leu	Glu	Gly	Arg	Trp	Arg	Leu	Leu	Asp	Ser

1	5	10	15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu	20	25	30
Gln Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp	35	40	45
Gly Arg Asn Leu Thr Thr Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln	50	55	60
Phe Ser Cys Thr Leu Gly Asp Glu Phe Glu Glu Thr Thr Ala Asp Gly	65	70	75
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln	85	90	95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys	100	105	110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr	115	120	125
Arg Ile Tyr Glu Lys Val Glu	130	135	

<210> 60  
 <211> 135  
 <212> PRT  
 <213> Bos taurus

<400> 60
Met Ala Thr Val Gln Gln Leu Val Gly Arg Trp Arg Leu Val Glu Ser
1 5 10 15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Val Gly Val Gly Met Ala Leu
20 25 30
Arg Lys Val Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Ser Asp
35 40 45
Gly Lys Asn Leu Ser Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60
Phe Ser Cys Lys Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Glu
100 105 110
Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125

Arg Val Tyr Glu Lys Val Glu  
130 135

<210> 61  
<211> 266  
<212> PRT  
<213> Homo sapiens

<400> 61

Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg  
20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln  
35 40 45

Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys  
50 55 60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn  
100 105 110

Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly  
130 135 140

Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg  
145 150 155 160

Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr  
165 170 175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu  
195 200 205

Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro  
210 215 220

Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser  
225 230 235 240

Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly  
245 250 255

Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro  
260 265

<210> 62  
<211> 265  
<212> PRT  
<213> Rattus norvegicus

<400> 62

Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg  
20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln  
35 40 45

Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys  
50 55 60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asp  
100 105 110

Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly  
130 135 140

Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg  
145 150 155 160

Val Val Ala Cys Ser Val Gln Pro Cys Pro His Thr Val Asp Cys Tyr  
165 170 175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Ala Tyr Leu  
195 200 205

Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Gln Lys Thr  
210 215 220

Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser  
225 230 235 240

Lys Gly His Pro Gln Asp Glu Ser Thr Val Leu Thr Lys Ala Gly Met

	245		250		255
Ala Thr Val Asp Ala Gly Val Tyr Pro					
	260		265		
<210> 63					
<211> 266					
<212> PRT					
<213> Mus musculus					
<400> 63					
Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr					
1		5		10	15
Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg					
	20		25		30
Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Asp Gln					
	35		40		45
Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys					
	50		55		60
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln					
65		70		75	80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala					
	85		90		95
Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asn					
	100		105		110
Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp					
	115		120		125
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly					
	130		135		140
Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg					
145		150		155	160
Val Val Ala Cys Ser Val Thr Pro Cys Pro His Thr Val Asp Cys Tyr					
	165		170		175
Ile Ala Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val					
	180		185		190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Val Tyr Leu					
	195		200		205
Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Arg Lys Ala					
	210		215		220
Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser					
225		230		235	240

Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly  
245 250 255

Met Ala Thr Val Asp Ala Gly Val Tyr Pro  
260 265

<210> 64

<211> 273

<212> PRT

<213> Homo sapiens

<400> 64

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His  
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys  
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn  
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala  
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro  
145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe  
165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu  
195 200 205

Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala  
210 215 220

Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln  
225 230 235 240

Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His  
245 250 255

Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile  
260 265 270

Leu

<210> 65

<211> 273

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (41)

<223> Wherein Xaa is any amino acid.

<400> 65

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Xaa Arg Val Trp Ser Asp Asp His  
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys  
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn  
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala  
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro  
145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe  
165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu  
 195 200 205  
 Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala  
 210 215 220  
 Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln  
 225 230 235 240  
 Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His  
 245 250 255  
 Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile  
 260 265 270

Leu

<210> 66  
 <211> 434  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Ala Lys Gln Gln Leu Asn Leu Arg Thr His Met Ala Asp Glu Asn Lys  
 1 5 10 15  
 Asn Glu Tyr Ala Ala Gln Leu Gln Asn Phe Asn Gly Glu Gln His Lys  
 20 25 30  
 His Phe Tyr Val Val Ile Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met  
 35 40 45  
 Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala  
 50 55 60  
 Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly  
 65 70 75 80  
 Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln Met  
 85 90 95  
 Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro  
 100 105 110  
 Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly Thr  
 115 120 125  
 Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr Thr  
 130 135 140  
 Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys  
 145 150 155 160  
 Pro Gln Ser Pro Pro Leu Thr Pro Thr Ser Leu Phe Thr Ser Ser Thr



165								170				175			
Pro	Asn	Gly	Ser	Gln	Phe	Leu	Thr	Phe	Ser	Ile	Glu	Pro	Val	His	Tyr
			180					185					190		
Cys	Met	Asn	Glu	Ile	Lys	Thr	Gly	Lys	Pro	Arg	Ile	Pro	Ser	Phe	Arg
		195					200					205			
Ser	Leu	Lys	Arg	Gly	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	Leu	Pro
	210					215					220				
Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Asn
225					230					235					240
Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	Lys	Met
				245					250					255	
Lys	Asp	Val	Tyr	Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu
			260						265				270		
Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met
		275					280					285			
Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr
	290					295					300				
Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val
305					310					315					320
Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn
				325					330					335	
Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe
			340						345				350		
Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys
		355					360					365			
Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met
	370					375					380				
Lys	Glu	Gly	Glu	Val	Leu	Tyr	Ile	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly
385					390					395					400
Trp	Thr	Arg	Ala	Arg	Arg	Gln	Asn	Gly	Glu	Glu	Gly	Tyr	Val	Pro	Thr
				405					410					415	
Ser	Tyr	Ile	Asp	Val	Thr	Leu	Glu	Lys	Asn	Ser	Lys	Gly	Ala	Val	Thr
			420						425				430		

Tyr Ile

<210> 67  
 <211> 330  
 <212> PRT

<213> Homo sapiens

<400> 67

Met	Asp	Glu	Arg	Arg	Thr	Ile	Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe	
1				5					10					15		
Ala	Asp	Ser	Glu	Arg	Lys	Val	Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu	
			20					25					30			
Gly	Met	Ile	Leu	Ala	Ala	Lys	Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln	
		35					40					45				
Met	Val	Val	Asp	Ser	Phe	Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	
	50					55					60					
Pro	Phe	Glu	Asp	Tyr	Ser	Gln	His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly	
65					70					75					80	
Thr	Ile	Ser	Ala	Ser	Lys	Gln	Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	
				85					90					95		
Thr	Val	Gly	Lys	Ala	Lys	Gly	Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	
		100						105					110			
Lys	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg	
		115					120					125				
Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Asn	Arg	Glu	Leu	Gln	
	130					135					140					
Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	Lys	Met	Lys	Asp	Val	Tyr	
145					150					155					160	
Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu	Gln	Pro	Lys	Leu	
				165					170					175		
Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met	Glu	Ile	His	Lys	
			180					185					190			
Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr	Gly	Gly	Arg	Gly	
		195					200					205				
Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val	Thr	Gln	Gly	Arg	
	210					215					220					
Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn	Gln	Glu	Val	Arg	
225					230					235					240	
Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe	Asp	Asp	Glu	Phe	
			245					250						255		
Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys	Lys	Ala	Ile	Tyr	
			260					265					270			
Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met	Lys	Glu	Gly	Glu	
		275					280					285				

Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala  
 290 295 300

Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp  
 305 310 315 320

Val Thr Leu Glu Lys Asn Ser Lys Gly Ser  
 325 330

<210> 68

<211> 592

<212> PRT

<213> Homo sapiens

<400> 68

Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys  
 1 5 10 15

His Thr Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val  
 20 25 30

Lys Glu Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn  
 35 40 45

Leu Ser Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu  
 50 55 60

Tyr Lys Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met  
 65 70 75 80

Asn Asp Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser  
 85 90 95

Gln Ile Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu  
 100 105 110

Arg Lys Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu  
 115 120 125

Thr Cys Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp  
 130 135 140

Cys Lys Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala  
 145 150 155 160

Asp Ile Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala  
 165 170 175

Gln Ile Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser  
 180 185 190

Ile Leu Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His  
 195 200 205

Ile Pro Asn Ile Phe Gln Lys Ile Gln Glu Met Glu Glu Arg Arg Ile  
 210 215 220

Val	Arg	Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	
225					230					235					240	
Val	Ile	Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	
				245					250					255		
Glu	Ser	Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	
			260					265					270			
Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	
		275					280					285				
Gln	Pro	Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	
	290					295					300					
Gly	Glu	Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	
305					310					315					320	
Leu	Trp	Pro	Phe	Ile	Lys	Lys	Asn	Lys	Ser	Pro	Lys	Gln	Gln	Lys	Glu	
				325					330					335		
Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	
			340					345					350			
His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	
		355					360					365				
Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	
	370					375					380					
Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	
385					390					395					400	
Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	
				405					410					415		
Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	
			420					425					430			
Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	
		435					440					445				
Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro	Ala	Arg	Asn	Glu	Gln	Ala	
	450					455					460					
Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	
465					470					475					480	
Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	
				485					490					495		
Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	
			500					505					510			
Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	
		515					520					525				

Leu	Tyr	Thr	Phe	Glu	Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu
530						535					540				
Gly	Glu	Thr	Leu	Tyr	Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr
545					550					555					560
Arg	Ile	Arg	Arg	Asn	Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr
				565					570					575	
Val	Glu	Val	Cys	Leu	Asp	Lys	Asn	Ala	Lys	Gly	Ala	Lys	Thr	Tyr	Ile
			580					585					590		

<210> 69  
 <211> 679  
 <212> PRT  
 <213> Homo sapiens

<400> 69															
Leu	Trp	Asn	Gly	Gly	Glu	Glu	Glu	Pro	Pro	Arg	Arg	Pro	Arg	Ala	Arg
1				5					10					15	
Ser	Cys	Glu	Pro	Glu	Glu	Ala	Ala	Arg	Thr	Pro	Gly	Phe	Pro	Pro	Ser
			20					25					30		
Arg	Gly	Ser	Arg	Gly	Ala	Lys	Gly	Ser	Pro	Gly	Arg	Gly	Thr	Arg	Glu
		35					40					45			
Pro	Arg	Pro	Pro	Arg	Gly	Ala	Pro	Leu	Arg	Val	Pro	Cys	Thr	Met	Ser
	50					55					60				
Trp	Gly	Thr	Glu	Leu	Trp	Asp	Gln	Phe	Asp	Asn	Leu	Glu	Lys	His	Thr
65				70					75						80
Gln	Trp	Gly	Ile	Asp	Ile	Leu	Glu	Lys	Tyr	Ile	Lys	Phe	Val	Lys	Glu
				85					90					95	
Arg	Thr	Glu	Ile	Glu	Leu	Ser	Tyr	Ala	Lys	Gln	Leu	Arg	Asn	Leu	Ser
		100						105					110		
Lys	Lys	Tyr	Gln	Pro	Lys	Lys	Asn	Ser	Lys	Glu	Glu	Glu	Glu	Tyr	Lys
		115					120					125			
Tyr	Thr	Ser	Cys	Lys	Ala	Phe	Ile	Ser	Asn	Leu	Asn	Glu	Met	Asn	Asp
	130					135					140				
Tyr	Ala	Gly	Gln	His	Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	Gln	Ile
145					150					155					160
Ile	Val	Asp	Leu	Ala	Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys
			165						170					175	
Ser	Asn	Phe	His	Asp	Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys

180							185					190						
Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys			
		195					200					205						
Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile			
	210					215					220							
Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile			
225					230					235					240			
Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu			
				245					250					255				
Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro			
			260					265					270					
Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg			
		275					280				285							
Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile			
	290					295					300							
Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser			
305					310					315					320			
Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser			
				325				330						335				
Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro			
			340					345					350					
Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu			
		355					360					365						
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp			
	370					375					380							
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His			
385					390					395					400			
Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro			
				405				410						415				
Asn	Gly	Pro	Gln	Ser	Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg			
			420					425					430					
Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser			
		435					440					445						
Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe			
	450					455					460							
Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val			
465					470					475					480			
Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala			

485					490					495					
Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp
			500						505				510		
Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu
		515					520					525			
Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val
	530					535					540				
Glu	Gly	Arg	Leu	Pro	Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly
545					550					555					560
Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp
				565					570					575	
Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	Gln	Ser	Gln	Glu	Ser
			580					585					590		
Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	Glu	Phe	Asp	Asp	Glu
		595					600					605			
Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	Leu	Tyr	Thr	Phe	Glu
	610					615					620				
Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu	Gly	Glu	Thr	Leu	Tyr
625					630					635					640
Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ile	Arg	Arg	Asn
				645					650					655	
Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr	Val	Glu	Val	Cys	Leu
			660					665					670		
Asp	Lys	Asn	Ala	Lys	Asp	Ser									
			675												

<210> 70  
 <211> 674  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
 Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu  
 1 5 10 15  
 Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly  
 20 25 30  
 Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg  
 35 40 45  
 Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu  
 50 55 60

Trp	Asp	Gln	Phe	Asp	Asn	Leu	Glu	Lys	His	Thr	Gln	Trp	Gly	Ile	Asp	
65					70					75					80	
Ile	Leu	Glu	Lys	Tyr	Ile	Lys	Phe	Val	Lys	Glu	Arg	Thr	Glu	Ile	Glu	
				85					90					95		
Leu	Ser	Tyr	Ala	Lys	Gln	Leu	Arg	Asn	Leu	Ser	Lys	Lys	Tyr	Gln	Pro	
			100					105						110		
Lys	Lys	Asn	Ser	Lys	Glu	Glu	Glu	Glu	Tyr	Lys	Tyr	Thr	Ser	Cys	Lys	
		115					120					125				
Ala	Phe	Ile	Ser	Asn	Leu	Asn	Glu	Met	Asn	Asp	Tyr	Ala	Gly	Gln	His	
	130					135					140					
Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	Gln	Ile	Ile	Val	Asp	Leu	Ala	
145					150					155					160	
Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys	Ser	Asn	Phe	His	Asp	
				165					170					175		
Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys	Trp	Lys	Gln	Leu	Glu	
			180					185					190			
Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	Glu	Ala	Asp	Arg	Ala	
		195					200					205				
Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	Asn	Val	Thr	Lys	Ala	
	210					215					220					
Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	Arg	His	Gln	Met	Ala	
225					230					235				240		
Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	Gln	Lys	Phe	Asn	His	
				245					250					255		
Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	Asn	Ile	Phe	Gln	Lys	
			260					265					270			
Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	Met	Gly	Glu	Ser	Met	
		275					280					285				
Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	Pro	Ile	Ile	Gly	Lys	
	290					295					300					
Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	Ile	Asp	Gln	Lys	Asn	
305					310					315					320	
Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	Gly	Phe	Glu	Pro	Pro	
				325					330					335		
Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	Met	Lys	Arg	Thr	Val	
			340					345					350			
Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	Gly	Lys	Pro	Asp	Leu	
		355					360					365				





Asp Ser

<210> 71  
<211> 457  
<212> PRT  
<213> Homo sapiens

<400> 71

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala  
1 5 10 15

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln  
20 25 30

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly  
35 40 45

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly  
50 55 60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile  
65 70 75 80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala  
85 90 95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe  
100 105 110

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln  
115 120 125

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly  
130 135 140

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys  
145 150 155 160

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala  
165 170 175

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro  
180 185 190

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu  
195 200 205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val  
210 215 220

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg  
225 230 235 240

His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala  
245 250 255

Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg  
 260 265 270  
 Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly  
 275 280 285  
 Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn  
 290 295 300  
 His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe  
 305 310 315 320  
 Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe  
 325 330 335  
 Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro  
 340 345 350  
 Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro Leu  
 355 360 365  
 Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala Leu  
 370 375 380  
 Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala  
 385 390 395 400  
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Asp Gly Asp Thr  
 405 410 415  
 Trp Arg Leu Val Gly Val Val Ser Trp Gly Arg Ala Cys Ala Glu Pro  
 420 425 430  
 Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile  
 435 440 445  
 His Asp Thr Ala Gln Asp Ser Leu Leu  
 450 455

<210> 72  
 <211> 455  
 <212> PRT  
 <213> Mus musculus

<400> 72  
 Met Ser Pro Thr Leu Asp Asp Gln Ser Pro Met Glu Ile Arg Cys Thr  
 1 5 10 15  
 Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg Met Glu Leu Gly Asp Gln  
 20 25 30  
 Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp Cys Cys Leu Gln Arg Gly  
 35 40 45  
 Cys Val Ile Leu Gly Val Leu Gly Leu Leu Ala Gly Ala Gly Ile Ala

50		55		60												
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Trp	Pro	Ala	Ala	Ser	Pro	Ser	Ile	
65					70					75					80	
Ser	Gly	Thr	Leu	Gln	Glu	Glu	Glu	Met	Thr	Leu	Asn	Cys	Pro	Gly	Val	
				85					90					95		
Ser	Cys	Glu	Glu	Glu	Leu	Leu	Pro	Ser	Leu	Pro	Lys	Thr	Val	Ser	Phe	
			100					105					110			
Arg	Ile	Asn	Gly	Glu	Asp	Leu	Leu	Leu	Gln	Val	Gln	Val	Arg	Ala	Arg	
		115					120					125				
Pro	Asp	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly	
						135					140					
Met	His	Ile	Cys	Lys	Ser	Leu	Gly	His	Ile	Arg	Leu	Thr	Gln	His	Lys	
145					150					155					160	
Ala	Val	Asn	Leu	Ser	Asp	Ile	Lys	Leu	Asn	Arg	Ser	Gln	Glu	Phe	Ala	
				165					170					175		
Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val	Glu	Glu	Ala	Trp	Lys	Pro	
			180					185					190			
Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val	Ser	Leu	Lys	Cys	Ser	Glu	
		195					200					205				
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ala	Val	
	210					215					220					
Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Met	Leu	Gly	Ser	Arg	
225					230					235					240	
His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro	His	Trp	Val	Val	Thr	Ala	
				245					250					255		
Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser	Arg	Leu	Ser	Ser	Trp	Arg	
			260					265					270			
Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala	Val	Arg	Gln	His	Gln	Gly	
		275					280					285				
Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn	
	290					295					300					
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	Arg	Thr	Pro	Ile	Asn	Phe	
305					310					315					320	
Ser	Asp	Thr	Val	Asp	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	Tyr	Phe	
				325					330					335		
Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	Asp	Pro	
			340					345					350			
Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln	Asp	Thr	Met	Val	Pro	Leu	

355	360	365
Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu		
370	375	380
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala		
385	390	395 400
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr		
	405	410 415
Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro		
	420	425 430
Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile		
	435	440 445
His Asp Thr Val Gln Val Arg		
450	455	

<210> 73  
 <211> 445  
 <212> PRT  
 <213> Mus musculus

<400> 73

Met Glu Ile Arg Cys Thr Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg
1 5 10 15
Met Glu Leu Gly Asp Gln Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp
20 25 30
Cys Cys Leu Gln Arg Gly Cys Val Ile Leu Gly Val Leu Gly Leu Leu
35 40 45
Ala Gly Ala Gly Ile Ala Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro
50 55 60
Ala Ala Ser Pro Ser Ile Ser Gly Thr Leu Gln Glu Glu Glu Met Thr
65 70 75 80
Leu Asn Cys Pro Gly Val Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu
85 90 95
Pro Lys Thr Val Ser Phe Arg Ile Asn Gly Glu Asp Leu Leu Leu Gln
100 105 110
Val Gln Val Arg Ala Arg Pro Asp Trp Leu Leu Val Cys His Glu Gly
115 120 125
Trp Ser Pro Ala Leu Gly Met His Ile Cys Lys Ser Leu Gly His Ile
130 135 140
Arg Leu Thr Gln His Lys Ala Val Asn Leu Ser Asp Ile Lys Leu Asn
145 150 155 160

Arg	Ser	Gln	Glu	Phe	Ala	Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val	165	170	175	
Glu	Glu	Ala	Trp	Lys	Pro	Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val	180	185	190	
Ser	Leu	Lys	Cys	Ser	Glu	Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	195	200	205	
Val	Gly	Gly	Gln	Ala	Val	Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	210	215	220	
Val	Met	Leu	Gly	Ser	Arg	His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro	225	230	235	240
His	Trp	Val	Val	Thr	Ala	Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser	245	250	255	
Arg	Leu	Ser	Ser	Trp	Arg	Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala	260	265	270	
Val	Arg	Gln	His	Gln	Gly	Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro	275	280	285	
Leu	Tyr	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	290	295	300	
Arg	Thr	Pro	Ile	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu	Pro	305	310	315	320
Ala	Lys	Glu	Gln	Tyr	Phe	Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly	325	330	335	
Trp	Gly	His	Thr	Asp	Pro	Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln	340	345	350	
Asp	Thr	Met	Val	Pro	Leu	Leu	Ser	Thr	His	Leu	Cys	Asn	Ser	Ser	Cys	355	360	365	
Met	Tyr	Ser	Gly	Ala	Leu	Thr	His	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu	370	375	380	
Asp	Gly	Arg	Ala	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	385	390	395	400
Cys	Pro	Ser	Gly	Asp	Thr	Trp	His	Leu	Val	Gly	Val	Val	Ser	Trp	Gly	405	410	415	
Arg	Gly	Cys	Ala	Glu	Pro	Asn	Arg	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala	420	425	430	
Glu	Phe	Leu	Asp	Trp	Ile	His	Asp	Thr	Val	Gln	Val	Arg				435	440	445	

<210> 74

<211> 398

<212> PRT

<213> Homo sapiens

<400> 74

Met	Ser	Leu	Met	Leu	Asp	Asp	Gln	Pro	Pro	Met	Glu	Ala	Gln	Tyr	Ala	
1				5					10					15		
Glu	Glu	Gly	Pro	Gly	Pro	Gly	Ile	Phe	Arg	Ala	Glu	Pro	Gly	Asp	Gln	
			20					25					30			
Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly	
		35					40					45				
Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly	
	50					55					60					
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile	
65					70					75					80	
Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala	
				85					90					95		
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe	
			100					105					110			
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln	
		115					120					125				
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly	
	130					135					140					
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys	
145					150					155					160	
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala	
				165					170					175		
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro	
			180					185					190			
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu	
		195					200					205				
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val	
	210					215					220					
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg	
225					230					235					240	
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala	
				245					250					255		
Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	Ala	Arg	Leu	Ser	Ser	Trp	Arg	
			260					265					270			
Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	Ala	Val	Arg	Pro	His	Gln	Gly	
		275					280					285				

Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn  
 290 295 300  
 His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe  
 305 310 315 320  
 Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe  
 325 330 335  
 Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro  
 340 345 350  
 Ser His Ser Leu Gln Leu Gly Tyr Ala Pro Gly His Gly Gly Ala Leu  
 355 360 365  
 Val Gln His Ser Ala Leu Gln Gln Leu Leu Arg Val Gln Arg Ser Pro  
 370 375 380  
 His Pro Pro His Ala Leu Arg Trp Leu Pro Gly Arg Lys Gly  
 385 390 395  
  
 <210> 75  
 <211> 311  
 <212> PRT  
 <213> Mus musculus  
  
 <400> 75  
 Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys  
 1 5 10 15  
 Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala  
 20 25 30  
 Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro  
 35 40 45  
 Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu  
 50 55 60  
 Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val  
 65 70 75 80  
 Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg  
 85 90 95  
 His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala  
 100 105 110  
 Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg  
 115 120 125  
 Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly  
 130 135 140  
 Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn



145		150		155		160
His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe						
	165			170		175
Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe						
	180			185		190
Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro						
	195			200		205
Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu						
	210			215		220
Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu						
	225			230		240
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala						
	245			250		255
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr						
	260			265		270
Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro						
	275			280		285
Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile						
	290			295		300
His Asp Thr Val Gln Val Arg						
	305			310		

<210> 76

<211> 199

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reprolysin  
family zinc protease Consensus Sequence

<400> 76

Lys Tyr Ile Glu Leu Phe Ile Val Val Asp His Gly Met Phe Thr Lys
1 5 10 15

Tyr Gly Ser Asp Leu Asn Lys Ile Arg Gln Arg Val His Gln Ile Val
20 25 30

Asn Leu Val Asn Glu Ile Tyr Arg Pro Leu Asn Ile Arg Val Val Leu
35 40 45

Val Gly Leu Glu Ile Trp Ser Asp Gly Asp Lys Ile Thr Val Gln Gly
50 55 60

Asp Ala Asn Asp Thr Leu His Arg Phe Leu Glu Trp Arg Glu Thr Asp
65 70 75 80

Leu Leu Lys Arg Lys Ser His Asp Asn Ala Gln Leu Leu Thr Gly Ile  
                     85                    90                    95  
 Asp Phe Asp Gly Asn Thr Ile Gly Ala Ala Tyr Val Gly Gly Met Cys  
                     100                    105                    110  
 Ser Pro Lys Arg Ser Val Gly Val Val Gln Asp His Ser Pro Ile Val  
                     115                    120                    125  
 Leu Leu Val Ala Val Thr Met Ala His Glu Leu Gly His Asn Leu Gly  
                     130                    135                    140  
 Met Thr His Asp Asp Ile Asn Lys Cys Thr Cys Glu Gly Gly Gly Gly  
                     145                    150                    155                    160  
 Cys Ile Met Asn Pro Val Ala Ser Ser Ser Pro Gly Lys Lys Phe Ser  
                     165                    170                    175  
 Asn Cys Ser Met Asp Asp Tyr Gln Gln Phe Leu Thr Lys Gly Lys Pro  
                     180                    185                    190  
 Gln Cys Leu Leu Asn Lys Pro  
                     195

<210> 77  
 <211> 51  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Thrombospondin  
           type 1 Consensus Sequence

<400> 77  
 Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly  
   1                    5                    10                    15  
 Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly  
                     20                    25                    30  
 Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln  
                     35                    40                    45  
 Pro Cys Pro  
           50

<210> 78  
 <211> 48  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Thrombospondin  
           type 1 domain Consensus Sequence

<400> 78

Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly  
1 5 10 15  
Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro  
20 25 30  
Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys  
35 40 45

<210> 79

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reprolysin  
family propeptide Consensus Sequence

<400> 79

His Leu Glu Lys Asn Arg Ser Leu Leu Ala Pro Asp Phe Thr Val Thr  
1 5 10 15  
Thr Tyr Asp Asp Asp Gly Thr Leu Val Thr Glu His Pro Leu Ile Gln  
20 25 30  
Asp His Cys Tyr Tyr Gln Gly Tyr Val Glu Gly Tyr Pro Asn Ser Ala  
35 40 45  
Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Leu Glu  
50 55 60  
Asn Leu Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ser Asp Gly Phe Glu  
65 70 75 80  
His Ile Ile Tyr Gln Ile Glu His Leu Lys Thr Val Pro Gly Pro Cys  
85 90 95  
Gly Glu Cys Gly Ser Leu Ser Val Ser Thr Asp Ser Gln Tyr Gly Ile  
100 105 110  
Arg Ser Pro Ser Pro  
115

<210> 80

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

# Alpha-2-macroglobulin family Consensus Sequence

<400> 80

Ile	Asp	Glu	Asp	Asp	Ile	Thr	Ile	Arg	Ser	Tyr	Phe	Pro	Glu	Ser	Trp	1	5	10	15
Leu	Trp	Glu	Val	Glu	Glu	Val	Asp	Arg	Ser	Pro	Val	Leu	Thr	Val	Asn	20	25	30	
Ile	Thr	Leu	Pro	Asp	Ser	Ile	Thr	Thr	Trp	Glu	Ile	Leu	Ala	Val	Ser	35	40	45	
Leu	Ser	Asn	Thr	Lys	Gly	Leu	Cys	Val	Ala	Asp	Pro	Val	Glu	Leu	Thr	50	55	60	
Val	Phe	Gln	Asp	Phe	Phe	Leu	Glu	Leu	Arg	Leu	Pro	Tyr	Ser	Val	Val	65	70	75	80
Arg	Gly	Glu	Gln	Val	Glu	Leu	Arg	Ala	Val	Leu	Tyr	Asn	Tyr	Leu	Pro	85	90	95	
Ser	Gln	Asp	Ile	Lys	Val	Val	Val	Gln	Leu	Glu	Val	Glu	Pro	Leu	Cys	100	105	110	
Gln	Ala	Gly	Phe	Cys	Ser	Leu	Ala	Thr	Gln	Arg	Thr	Arg	Ser	Ser	Gln	115	120	125	
Ser	Val	Arg	Pro	Lys	Ser	Leu	Ser	Ser	Val	Ser	Phe	Pro	Val	Val	Val	130	135	140	
Val	Pro	Leu	Ala	Ser	Gly	Leu	Ser	Leu	Val	Glu	Val	Val	Ala	Ser	Val	145	150	155	160
Pro	Glu	Phe	Phe	Val	Lys	Asp	Ala	Val	Val	Lys	Thr	Leu	Lys	Val	Glu	165	170	175	
Pro	Glu	Gly	Ala	Arg	Lys	Glu	Glu	Thr	Val	Ser	Ser	Leu	Leu	Leu	Pro	180	185	190	
Pro	Glu	His	Leu	Gly	Gly	Gly	Leu	Glu	Val	Ser	Glu	Val	Pro	Ala	Leu	195	200	205	
Lys	Leu	Pro	Asp	Asp	Val	Pro	Asp	Thr	Glu	Ala	Glu	Ala	Val	Ile	Ser	210	215	220	
Val	Gln	Gly	Asp	Pro	Val	Ala	Gln	Ala	Ile	Gln	Asn	Thr	Leu	Ser	Gly	225	230	235	240
Glu	Gly	Leu	Asn	Asn	Leu	Leu	Arg	Leu	Pro	Ser	Gly	Cys	Gly	Glu	Gln	245	250	255	
Asn	Met	Ile	Tyr	Met	Ala	Pro	Thr	Val	Tyr	Val	Leu	His	Tyr	Leu	Asp	260	265	270	
Glu	Thr	Trp	Gln	Trp	Glu	Lys	Pro	Gly	Thr	Lys	Lys	Lys	Gln	Lys	Ala	275	280	285	

Ile	Asp	Leu	Ile	Asn	Lys	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Arg	Lys	290	295	300	
Ala	Asp	Gly	Ser	Tyr	Ala	Ala	Phe	Leu	His	Arg	Ala	Ser	Ser	Thr	Trp	305	310	315	320
Leu	Thr	Ala	Phe	Val	Leu	Lys	Val	Phe	Ser	Gln	Ala	Arg	Asn	Tyr	Val	325	330	335	
Phe	Ile	Asp	Glu	Glu	His	Ile	Cys	Gly	Ala	Val	Lys	Trp	Leu	Ile	Leu	340	345	350	
Asn	Gln	Gln	Lys	Asp	Asp	Gly	Val	Phe	Arg	Glu	Ser	Gly	Pro	Val	Ile	355	360	365	
His	Asn	Glu	Met	Lys	Gly	Gly	Val	Gly	Asp	Asp	Ala	Glu	Val	Glu	Val	370	375	380	
Thr	Leu	Thr	Ala	Phe	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ala	Lys	Leu	Val	385	390	395	400
Cys	Ile	Ser	Pro	Val	Val	Ala	Asn	Ala	Leu	Ser	Ile	Leu	Lys	Ala	Ser	405	410	415	
Asp	Tyr	Leu	Leu	Glu	Asn	Tyr	Ala	Asn	Gly	Gln	Arg	Val	Tyr	Thr	Leu	420	425	430	
Ala	Leu	Thr	Ala	Tyr	Ala	Leu	Ala	Leu	Ala	Gly	Val	Leu	His	Lys	Leu	435	440	445	
Lys	Glu	Ile	Leu	Lys	Ser	Leu	Lys	Glu	Glu	Leu	Tyr	Lys	Ala	Leu	Val	450	455	460	
Lys	Gly	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Asp	Ala	Pro	Gly	His	465	470	475	480
Pro	Tyr	Ser	Pro	Gln	Pro	Gln	Ala	Ala	Ala	Val	Glu	Met	Thr	Ser	Tyr	485	490	495	
Ala	Leu	Leu	Ala	Leu	Leu	Thr	Leu	Leu	Pro	Phe	Pro	Lys	Val	Glu	Met	500	505	510	
Ala	Pro	Lys	Val	Val	Lys	Trp	Leu	Thr	Glu	Gln	Gln	Tyr	Tyr	Gly	Gly	515	520	525	
Gly	Phe	Gly	Ser	Thr	Gln	Asp	Thr	Val	Met	Ala	Leu	Gln	Ala	Leu	Ser	530	535	540	
Lys	Tyr	Gly	Ile	Ala	Thr	Pro	Thr	His	Lys	Glu	Lys	Asn	Leu	Ser	Val	545	550	555	560
Thr	Ile	Gln	Ser	Pro	Ser	Gly	Ser	Phe	Lys	Ser	His	Phe	Gln	Ile	Leu	565	570	575	
Asn	Asn	Asn	Ala	Phe	Leu	Leu	Arg	Pro	Val	Glu	Leu	Pro	Leu	Asn	Glu	580	585	590	

Gly Phe Thr Val Thr Ala Lys Val Thr Gly Gln Gly Thr Leu Thr Leu  
 595 600 605  
 Val Thr Thr Tyr Arg Tyr Lys Val Leu Asp Lys Lys Asn Thr Phe Cys  
 610 615 620  
 Phe Asp Leu Lys Ile Glu Thr Val Pro Asp Thr Cys Val Glu Pro Lys  
 625 630 635 640  
 Gly Ala Lys Asn Ser Asp Tyr Leu Ser Ile Cys Thr Arg Tyr Ala Gly  
 645 650 655  
 Ser Arg Ser Asp Ser Gly Met Ala Ile Ala Asp Ile Ser Met Leu Thr  
 660 665 670  
 Gly Phe Ile Pro Leu Lys Pro Asp Leu Lys Lys Leu Glu Asn Gly Val  
 675 680 685  
 Asp Arg Tyr Val Ser Lys Tyr Glu Ile Asp Gly Asn His Val Leu Leu  
 690 695 700  
 Tyr Leu Asp Lys Val Ser His Ser Glu Thr Glu Cys Val Gly Phe Lys  
 705 710 715 720  
 Ile His Gln Asp Phe Glu Val Gly Leu Leu Gln Pro Ala Ser Val Lys  
 725 730 735  
 Val Tyr Asp Tyr Tyr Glu Pro Asp Glu Gln Cys Thr Ala Phe Tyr  
 740 745 750

<210> 81  
 <211> 620  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Alpha-2-macroglobulin family N-terminal region  
 Consensus Sequence

<400> 81  
 Arg Leu Leu Trp Leu Leu Leu Leu Leu Leu Phe Phe Asp Ser Ser  
 1 5 10 15  
 Leu Gln Lys Pro Arg Tyr Met Val Ile Val Pro Ser Ile Leu Arg Thr  
 20 25 30  
 Glu Thr Pro Glu Lys Val Cys Val Gln Leu His Asp Leu Asn Glu Thr  
 35 40 45  
 Val Thr Val Thr Val Ser Leu His Ser Phe Pro Gly Lys Arg Asn Leu  
 50 55 60  
 Ser Ser Leu Phe Thr Val Leu Leu Ser Ser Lys Asp Leu Phe His Cys  
 65 70 75 80

Val	Ser	Phe	Thr	Val	Pro	Gln	Pro	Gly	Leu	Phe	Lys	Ser	Ser	Lys	Gly			
				85					90					95				
Glu	Glu	Ser	Phe	Val	Val	Val	Gln	Val	Lys	Gly	Pro	Thr	His	Thr	Phe			
			100					105					110					
Lys	Glu	Lys	Val	Thr	Val	Leu	Val	Ser	Ser	Arg	Arg	Gly	Leu	Val	Phe			
		115					120					125						
Ile	Gln	Thr	Asp	Lys	Pro	Ile	Tyr	Thr	Pro	Gly	Gln	Thr	Val	Arg	Tyr			
	130					135					140							
Arg	Val	Phe	Ser	Val	Asp	Glu	Asn	Leu	Arg	Pro	Leu	Asn	Glu	Leu	Ile			
145					150					155					160			
Leu	Val	Tyr	Ile	Glu	Asp	Pro	Glu	Gly	Asn	Arg	Val	Asp	Gln	Trp	Glu			
				165				170						175				
Val	Asn	Lys	Leu	Glu	Gly	Gly	Ile	Phe	Gln	Leu	Ser	Phe	Pro	Ile	Pro			
			180					185					190					
Ser	Glu	Pro	Ile	Gln	Gly	Thr	Trp	Lys	Ile	Val	Ala	Arg	Tyr	Glu	Ser			
		195					200					205						
Gly	Pro	Glu	Ser	Asn	Tyr	Thr	His	Tyr	Phe	Glu	Val	Lys	Glu	Tyr	Val			
	210					215					220							
Leu	Pro	Ser	Phe	Glu	Val	Ser	Ile	Thr	Pro	Pro	Lys	Pro	Phe	Ile	Tyr			
225					230				235						240			
Tyr	Asp	Asn	Phe	Lys	Glu	Phe	Glu	Val	Thr	Ile	Cys	Ala	Arg	Tyr	Thr			
			245					250						255				
Tyr	Gly	Lys	Pro	Val	Pro	Gly	Val	Ala	Tyr	Val	Arg	Phe	Gly	Val	Lys			
			260					265					270					
Asp	Glu	Asp	Gly	Lys	Lys	Glu	Leu	Leu	Ala	Gly	Leu	Glu	Glu	Arg	Ala			
		275					280					285						
Lys	Leu	Leu	Asp	Gly	Asn	Gly	Glu	Ile	Cys	Leu	Ser	Gln	Glu	Val	Leu			
	290					295					300							
Leu	Lys	Glu	Leu	Gln	Leu	Lys	Asn	Glu	Asp	Leu	Glu	Gly	Lys	Ser	Leu			
305					310				315						320			
Tyr	Val	Ala	Val	Ala	Val	Ile	Glu	Ser	Glu	Gly	Gly	Asp	Met	Glu	Glu			
				325				330					335					
Ala	Glu	Leu	Gly	Gly	Ile	Lys	Ile	Val	Arg	Ser	Pro	Tyr	Lys	Leu	Lys			
			340				345						350					
Phe	Val	Lys	Thr	Pro	Ser	His	Phe	Lys	Pro	Gly	Ile	Pro	Phe	Phe	Leu			
		355					360					365						
Lys	Val	Leu	Val	Val	Asp	Pro	Asp	Gly	Ser	Pro	Ala	Pro	Asn	Val	Pro			
	370					375					380							

Val	Lys	Val	Ser	Ala	Gln	Asp	Ala	Ser	Tyr	Tyr	Ser	Asn	Gly	Thr	Thr	
385					390					395					400	
Asp	Glu	Asp	Gly	Leu	Ala	Gln	Phe	Ser	Ile	Asn	Thr	Ser	Gly	Ile	Ser	
				405					410					415		
Ser	Leu	Ser	Ile	Thr	Val	Arg	Thr	Asn	His	Lys	Glu	Leu	Pro	Glu	Glu	
			420					425					430			
Val	Gln	Ala	His	Ala	Glu	Ala	Gln	Ala	Thr	Ala	Tyr	Ser	Thr	Val	Ser	
		435					440					445				
Leu	Ser	Lys	Ser	Tyr	Ile	His	Leu	Ser	Ile	Glu	Arg	Thr	Leu	Pro	Cys	
	450					455					460					
Gly	Pro	Gly	Val	Gly	Glu	Gln	Ala	Asn	Phe	Ile	Leu	Arg	Gly	Lys	Ser	
465					470					475					480	
Leu	Gly	Glu	Leu	Lys	Ile	Leu	His	Phe	Tyr	Tyr	Leu	Ile	Met	Ser	Lys	
				485					490					495		
Gly	Lys	Ile	Val	Lys	Thr	Gly	Arg	Glu	Pro	Arg	Glu	Pro	Gly	Gln	Gly	
			500					505					510			
Leu	Phe	Ser	Leu	Ser	Ile	Pro	Val	Thr	Pro	Asp	Leu	Ala	Pro	Ser	Phe	
		515					520					525				
Arg	Leu	Val	Ala	Tyr	Tyr	Ile	Leu	Pro	Gln	Gly	Glu	Val	Val	Ala	Asp	
	530					535					540					
Ser	Val	Trp	Ile	Asp	Val	Glu	Asp	Cys	Cys	Ala	Asn	Lys	Leu	Asp	Leu	
545					550					555					560	
Ser	Phe	Ser	Pro	Ser	Lys	Asp	Tyr	Arg	Leu	Pro	Ala	Gln	Gln	Val	Lys	
				565					570					575		
Leu	Arg	Val	Glu	Ala	Asp	Pro	Gln	Ser	Leu	Val	Ala	Leu	Arg	Ala	Val	
			580					585					590			
Asp	Gln	Ala	Val	Tyr	Leu	Leu	Lys	Pro	Lys	Ala	Lys	Leu	Ser	Met	Ser	
		595					600					605				
Lys	Val	Tyr	Asp	Leu	Leu	Glu	Lys	Ser	Asp	Leu	Gly					
	610					615					620					

<210> 82  
 <211> 186  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sodium Bile  
 acid symporter family consensus sequence

<400> 82  
 Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg



1	5	10	15
Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu	20	25	30
Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu	35	40	45
Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile	50	55	60
Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr	65	70	75
Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser	85	90	95
Thr Leu Leu Ala Pro Leu Val Thr Pro Leu Leu Ser Phe Leu Leu Ala	100	105	110
Gly Leu Leu Val His Val Asp Ala Val Ser Pro Trp Ser Leu Ile Lys	115	120	125
Ser Val Leu Val Tyr Val Ile Ile Pro Leu Ile Ala Gly Met Leu Thr	130	135	140
Arg Tyr Phe Leu Pro Glu Trp Phe Glu Gln Arg Val Leu Pro Val Leu	145	150	155
Ser Pro Ile Ser Leu Ile Gly Leu Leu Leu Thr Ile Val Val Ile Phe	165	170	175
Ala Leu Asn Gly Glu Val Ile Ala Ser Leu	180	185	

<210> 83

<211> 191

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SPFH  
domain/Band 7 family Consensus Sequence

<400> 83

Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val	1	5	10	15
Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg	20	25	30	
Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe	35	40	45	
Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val	50	55	60	

Pro	Ser	Gln	Glu	Ile	Ile	Thr	Lys	Asp	Asn	Val	Val	Val	Ile	Val	Asp	65	70	75	80
Ala	Val	Val	Tyr	Tyr	Arg	Val	Val	Asp	Pro	Leu	Lys	Ala	Val	Tyr	Glu	85	90	95	
Val	Glu	Asp	Ala	Glu	Arg	Ala	Leu	Pro	Gln	Leu	Ala	Gln	Thr	Thr	Leu	100	105	110	
Arg	Asn	Val	Ile	Gly	Gln	Phe	Thr	Leu	Asp	Glu	Ile	Leu	Thr	Glu	Arg	115	120	125	
Glu	Arg	Ile	Asn	Ser	Gln	Leu	Arg	Glu	Ile	Leu	Asp	Glu	Ala	Thr	Asp	130	135	140	
Pro	Trp	Gly	Ile	Lys	Val	Glu	Arg	Val	Glu	Ile	Lys	Asp	Ile	Arg	Leu	145	150	155	160
Pro	Glu	Glu	Val	Gln	Arg	Ala	Met	Ala	Ala	Gln	Met	Glu	Ala	Glu	Arg	165	170	175	
Glu	Ala	Arg	Ala	Lys	Ile	Leu	Glu	Ala	Glu	Gly	Glu	Gln	Glu	Ala		180	185	190	

<210> 84

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Prohibitin  
homologues Consensus Sequence

<400> 84

Ala	Ala	Phe	Tyr	Val	Ile	Gly	Glu	Gly	Glu	Arg	Gly	Val	Val	Glu	Arg	1	5	10	15
Leu	Gly	Arg	Val	Leu	Lys	Val	Leu	Gly	Pro	Gly	Leu	His	Phe	Val	Ile	20	25	30	
Pro	Phe	Ile	Asp	Asp	Val	Lys	Arg	Val	Asp	Leu	Arg	Ala	Gln	Thr	Asp	35	40	45	
Asp	Val	Pro	Pro	Gln	Glu	Val	Ile	Thr	Lys	Asp	Asn	Val	Thr	Val	Ser	50	55	60	
Val	Asp	Ala	Val	Val	Tyr	Tyr	Arg	Val	Leu	Asp	Pro	Leu	Lys	Ala	Val	65	70	75	80
Tyr	Gly	Val	Leu	Asp	Ala	Asp	Tyr	Arg	Ala	Leu	Arg	Gln	Leu	Ala	Gln	85	90	95	
Thr	Thr	Leu	Arg	Ser	Val	Ile	Gly	Lys	Arg	Thr	Leu	Asp	Glu	Leu	Leu	100	105	110	

Thr Asp Glu Arg Glu Lys Ile Ser Glu Asn Ile Arg Glu Glu Leu Asn  
115 120 125

Glu Ala Ala Glu Pro Trp Gly Ile Glu Val Glu Asp Val Glu Ile Lys  
130 135 140

Asp Ile Arg Leu Pro Glu Glu Ile Lys Glu Ala Met Glu Ala Gln Gln  
145 150 155 160

<210> 85

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain  
Consensus Sequence

<400> 85

Cys Tyr His Gly Asn Gly Glu Asn Tyr Arg Gly Thr Ala Ser Thr Thr  
1 5 10 15

Glu Ser Gly Ala Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro His Arg  
20 25 30

His Ser Lys Tyr Thr Pro Glu Arg Tyr Pro Ala Lys Gly Leu Gly Glu  
35 40 45

Asn Tyr Cys Arg Asn Pro Asp Gly Asp Glu Arg Pro Trp Cys Tyr Thr  
50 55 60

Thr Asp Pro Arg Val Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys  
65 70 75

<210> 86

<211> 83

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain  
Consensus Sequence

<400> 86

Arg Asp Cys Tyr Ala Gly Asn Gly Glu Ser Tyr Arg Gly Thr Ala Ser  
1 5 10 15

Thr Thr Lys Ser Gly Lys Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro  
20 25 30

His Leu His Arg Phe Thr Pro Glu Arg Phe Pro Glu Leu Gly Leu Glu  
35 40 45

His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ser Glu Gly Pro Trp Cys  
50 55 60

Tyr Thr Thr Asp Pro Asn Val Arg Trp Glu Tyr Cys Asp Ile Pro Gln  
65 70 75 80

Cys Glu Ser

<210> 87

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like  
serine protease Consensus Sequence

<400> 87

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln  
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu  
20 25 30

Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser  
35 40 45

Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser  
50 55 60

Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro  
65 70 75 80

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu  
85 90 95

Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro  
100 105 110

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly  
115 120 125

Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln  
130 135 140

Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr  
145 150 155 160

Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu  
165 170 175

Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
180 185 190

Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser  
 195 200 205

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser  
 210 215 220

Ser Tyr Leu Asp Trp Ile  
 225 230

<210> 88

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin  
 Consensus Sequence

<400> 88

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val  
 1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser  
 20 25 30

Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser  
 35 40 45

Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr  
 50 55 60

Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn  
 65 70 75 80

Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr  
 85 90 95

Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp  
 100 105 110

Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys  
 115 120 125

Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val  
 130 135 140

Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr  
 145 150 155 160

Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp  
 165 170 175

Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val  
 180 185 190

Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr

195	200	205
Arg Val Ser Arg Tyr Leu Asp Trp Ile		
210	215	

<210> 89  
 <211> 79  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Divergent  
 subfamily of APPLE domains Consensus Sequence

<400> 89  
 Lys Ser Asp Asp Cys Phe Val Arg Leu Pro Asn Thr Lys Leu Pro Asp  
 1 5 10 15  
 Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln  
 20 25 30  
 Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn  
 35 40 45  
 Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala  
 50 55 60  
 Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile  
 65 70 75

<210> 90  
 <211> 145  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 Lipocalin/cytosolic fatty-acid binding protein  
 family Consensus Sequence

<400> 90  
 Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro  
 1 5 10 15  
 Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile  
 20 25 30  
 Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys  
 35 40 45  
 Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys  
 50 55 60  
 Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val  
 65 70 75 80

Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly  
85 90 95

Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro  
100 105 110

Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu  
115 120 125

Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg  
130 135 140

Cys  
145

<210> 91  
<211> 218  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Connexin  
Consensus Sequence

<400> 91

Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His  
1 5 10 15

Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg  
20 25 30

Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln  
35 40 45

Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys  
50 55 60

Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln  
65 70 75 80

Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala  
85 90 95

Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His  
100 105 110

Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu  
115 120 125

Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe  
130 135 140

Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln  
145 150 155 160

Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg  
 165 170 175  
 Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu  
 180 185 190  
 Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu  
 195 200 205  
 Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu  
 210 215

<210> 92  
 <211> 59  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Src homology 3  
 domains Consensus Sequence

<400> 92  
 Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro  
 1 5 10 15  
 Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys  
 20 25 30  
 Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly  
 35 40 45  
 Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp  
 50 55

<210> 93  
 <211> 57  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: SH3 domain  
 Consensus Sequence

<400> 93  
 Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu  
 1 5 10 15  
 Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp  
 20 25 30  
 Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu  
 35 40 45  
 Ile Pro Ser Asn Tyr Val Glu Pro Val  
 50 55



<210> 94  
 <211> 91  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fes/CIP4  
 homology domain Consensus Sequence

<400> 94  
 Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser  
   1                  5                  10                  15  
 Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met  
                   20                  25                  30  
 Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys  
           35                  40                  45  
 Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly  
       50                  55                  60  
 Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu  
   65                  70                  75                  80  
 Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu  
                   85                  90

<210> 95  
 <211> 94  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fes/CIP4  
 homology domain Consensus Sequence

<400> 95  
 Met Gly Phe Gly Ser Glu Leu Cys Pro Glu Gly His Lys Ala Leu Leu  
   1                  5                  10                  15  
 Ser Arg Gln Asp Asn Glu Leu Arg Leu Leu Glu Glu Met Lys Lys Phe  
           20                  25                  30  
 Met Ala Glu Arg Ala Lys Ile Glu Lys Glu Tyr Ala Gly Lys Leu Gln  
       35                  40                  45  
 His Leu Ser Ala Gln Val Gly Lys Gly Pro Ala Thr Ala Glu Gly Glu  
       50                  55                  60  
 Asp Glu Leu Ser Ser Leu Lys Ser Trp Ala Val Ile Leu Ser Glu Thr  
   65                  70                  75                  80  
 Glu Gln Gln Ser Lys Ile His Leu Gln Ile Ser Glu Asp Leu

<220>  
<223> Description of Artificial Sequence: Trypsin-like  
serine protease Consensus Sequence

[illegible]

<210> 97  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Trypsin  
 Consensus Sequence

<400> 97  
 Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val  
   1                  5                  10                  15  
 Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser  
           20                  25                  30  
 Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser  
           35                  40                  45  
 Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr  
           50                  55                  60  
 Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn  
   65                  70                  75                  80  
 Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr  
                   85                  90                  95  
 Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp  
           100                  105                  110  
 Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys  
           115                  120                  125  
 Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val  
           130                  135                  140  
 Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr  
   145                  150                  155                  160  
 Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp  
           165                  170                  175  
 Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val  
           180                  185                  190  
 Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr  
           195                  200                  205  
 Arg Val Ser Arg Tyr Leu Asp Trp Ile  
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<210> 98  
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 ctcccactcc tgctgcttct gact 24  
  
 <210> 99  
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 aaggctgggc ctaaccagc ctcac 25  
  
 <210> 100  
 <211> 23  
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 <400> 100  
 catgaactgg gcatttctgc agg 23  
  
 <210> 101  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 ttatctgctg atctcgagg ttatgga 27  
  
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 <400> 102  
 ctgacaggcc ctggtgtgtg at 22

<210> 103  
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 actcatgcaa cttgcttctc tcactct 27  
  
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 <210> 107  
 <211> 25  
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<400> 107  
aggactcaga ggagggagtc ctgag 25

<210> 108  
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<220>  
<223> Description of Artificial Sequence: Ag4164 Forward

<400> 108  
gcactacaag tggaagcctt ac 22

<210> 109  
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<220>  
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 109  
ctcaagtaga agccgactta tgcaaa 26

<210> 110  
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<220>  
<223> Description of Artificial Sequence: Ag4164 Reverse

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tcaaadcctt ctgcgataca gt 22

<210> 111  
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<220>  
<223> Description of Artificial Sequence: Ag1313b  
Forward

<400> 111  
cagctgcacg attaataag at 22

<210> 112  
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<212> DNA  
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<210> 113  
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 Reverse  
  
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 ccaaagttgt gtccagactc at 22

<210> 114  
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 <400> 114  
 ccaaggaaga cctcttcatc tt 22

<210> 115  
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 tcttgcttac ggcataagcg ctctct 26

<210> 116  
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 <223> Description of Artificial Sequence: Ag2197 Reverse  
  
 <400> 116  
 ttcatttcta tgggacctca ga 22

<210> 117  
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 <223> Description of Artificial Sequence: Ag708 Forward  
  
 <400> 117  
 aaagatggga ctcgtcatga c 21  
  
 <210> 118  
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 <400> 118  
 cacgccatct tactgactgg tctgga 26  
  
 <210> 119  
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 <220>  
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 <210> 120  
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 <400> 120  
 gcactacaag tggaagcctt ac 22  
  
 <210> 121  
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 <212> DNA  
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<400> 121  
 ctcaagtaga agccgactta tgcaaa 26

<210> 122  
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<220>  
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<400> 122  
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<210> 123  
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<220>  
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<400> 123  
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<210> 124  
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<220>  
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<400> 124  
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<210> 125  
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<220>  
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<400> 125  
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<210> 126  
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<220>  
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 <400> 126  
 ccaaggaaga cctcttcatc tt 22  
  
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 <220>  
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 <400> 129  
 aaagatggga ctcgtcatga c 21  
  
 <210> 130  
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 cacgccatct tactgactgg tctgga 26  
  
 <210> 131

<211> 20  
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 <223> Description of Artificial Sequence: Ag708 Reverse  
  
 <400> 131  
 gtgcaaattcc caaagtgtca 20

<210> 132  
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 Forward  
  
 <400> 132  
 cagctgcacg attaatgaag at 22

<210> 133  
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 <400> 133  
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<210> 134  
 <211> 22  
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 Reverse  
  
 <400> 134  
 ccaaagttgt gtccagactc at 22

<210> 135  
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 <223> Description of Artificial Sequence: Ag1537 Forward

<400> 135  
tttcaagaca ccctgtgata cc 22

<210> 136  
<211> 26  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag1537 Probe

<400> 136  
acttcgtgtc ctgaatgttc caggct 26

<210> 137  
<211> 22  
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<220>  
<223> Description of Artificial Sequence: Ag1537 Reverse

<400> 137  
cagaggaatg aaggcataga tg 22

<210> 138  
<211> 21  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag2432 Forward

<400> 138  
gtaggcaaag ggactcactg t 21

<210> 139  
<211> 26  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag2432 Probe

<400> 139  
cagaaatcaa taatctttga ctgccg 26

<210> 140  
<211> 19  
<212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Ag2432 Reverse  
  
 <400> 140  
 gcacattacg tggctgaga 19  
  
 <210> 141  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag1250 Forward  
  
 <400> 141  
 cgtggtgaac tctgccttat at 22  
  
 <210> 142  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Ag1250 Probe  
  
 <400> 142  
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 <210> 143  
 <211> 21  
 <212> DNA  
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 <400> 143  
 agtccctttg cctaccacaa t 21  
  
 <210> 144  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag3086 Forward  
  
 <400> 144  
 ggacccatt cgactactgt 20  
  
 <210> 145  
 <211> 23

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag3086 Probe  
  
 <400> 145  
 ctgatgacca gccgccatca atc 23  
  
 <210> 146  
 <211> 20  
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 <220>  
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 <400> 146  
 ttctcaaact gcacctggtc 20  
  
 <210> 147  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag3797 Forward  
  
 <400> 147  
 tctggacgac aactattgcc 20  
  
 <210> 148  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Ag3797 Probe  
  
 <400> 148  
 atggtgctac actacggatc cgcag 25  
  
 <210> 149  
 <211> 20  
 <212> DNA  
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 <223> Description of Artificial Sequence: Ag3797 Reverse  
  
 <400> 149  
 gtcacagaat tctcgctcga 20

<210> 150  
 <211> 22  
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 <220>  
 <223> Description of Artificial Sequence: Ag2439 Forward  
  
 <400> 150  
 tatcatcact tgtgatggca aa 22  
  
 <210> 151  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Ag2439 Probe  
  
 <400> 151  
 aaaaccgaga gcactttgaa aacaca 26  
  
 <210> 152  
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 <400> 152  
 aaacttctct cccagggtac aa 22  
  
 <210> 153  
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 <223> Description of Artificial Sequence: Ag2771 Forward  
  
 <400> 153  
 tgaacagaac tatgcgaaac aa 22  
  
 <210> 154  
 <211> 27  
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 <220>  
 <223> Description of Artificial Sequence: Ag2771 Probe

<400> 154  
tctgggtaag aagtactgcc ccaaacg 27

<210> 155  
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<220>  
<223> Description of Artificial Sequence: Ag2771 Reverse

<400> 155  
ggctcttcat ctttgatga a 21

<210> 156  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1674 Forward

<400> 156  
ctcactcacc acaaggaggt aa 22

<210> 157  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1674 Probe

<400> 157  
tgacatcaaa ctcaacagtt cccagga 27

<210> 158  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1674 Reverse

<400> 158  
gtctaggaga gagctgagca aa 22

<210> 159  
<211> 78  
<212> PRT  
<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence: PAN domain  
Consensus Sequence

<400> 159

Cys Ser Ser Phe Val Arg Val Pro Gly Arg Ser Leu Ser Gly Asn Asp  
1 5 10 15

Ile Ser Val Val Asn Val Pro Ser Leu Glu Glu Cys Ala Ala Leu Cys  
20 25 30

Leu Glu Glu Pro Arg Val Cys Arg Ser Phe Thr Tyr Asn Asn Lys Ser  
35 40 45

Lys Gln Cys Leu Leu Lys Ser Glu Ser Ser Gly Ser Leu Pro Arg Leu  
50 55 60

Lys Arg Pro Ser Gln Lys Val Asp Tyr Tyr Glu Lys Ser Cys  
65 70 75

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin  
homologues Consensus Sequence

<400> 160

Ser Val Trp Gly Asp Glu Gln Ser Asp Phe Thr Cys Asn Thr Gln Gln  
1 5 10 15

Pro Gly Cys Glu Asn Val Cys Tyr Asp Gln Phe Phe Pro Ile Ser His  
20 25 30

Val Arg

<210> 161

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 161

Asn Glu Gln Lys  
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<210> 162

<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:

<400> 162

Asn His Gln Lys  
1

<210> 163  
<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:

<400> 163

Asn Asp Glu Gln  
1

<210> 164  
<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:

<400> 164

Gln His Arg Lys  
1

<210> 165  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:

<400> 165

Met Ile Leu Val  
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<210> 166  
<211> 4  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:

<400> 166

Met Ile Leu Phe  
1